

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2004, 04:28:27 ; Search time 78 Seconds

(without alignments)
2835.038 Million cell updates/sec

Title: US-09-315-355C-10

Perfect score: 501
Sequence: 1 MNRSRQVTCVAMVRCGVAKC.....RNSISGPGSRSSDTMES 501

Scoring table:

OLIGO	Xgapop 60.0	Xgapext 60.0
	Ygapop 60.0	Ygapext 60.0
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135299

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -OPMT=fastcap -SUFFIX=olip2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09315355 @CGN 1.1 85 @runat.30012004.091942.24664 -NCPU=6 -ICPU=3
-NO MMAR -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARR_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Issued Patents NA:*

- 1: /cgnt2_6/ptodata/2/ina/5A.COMB.seq:*
- 2: /cgnt2_6/ptodata/2/ina/5B.COMB.seq:*
- 3: /cgnt2_6/ptodata/2/ina/6A.COMB.seq:*
- 4: /cgnt2_6/ptodata/2/ina/6B.COMB.seq:*
- 5: /cgnt2_6/ptodata/2/ina/PTUS.COMB.seq:*
- 6: /cgnt2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	10	2.0	555	4 US-09-449-285A-15	Sequence 15, Appli
C 2	10	2.0	10380	3 US-09-077-354B-3	Sequence 23, Appli
C 3	9	1.8	321	2 US-08-520-678A-23	Sequence 23, Appli
C 4	9	1.8	321	3 US-08-897-126-23	Sequence 23, Appli
C 5	9	1.8	356	2 US-08-520-678A-22	Sequence 22, Appli
C 6	9	1.8	356	3 US-08-897-126-22	Sequence 22, Appli
C 7	9	1.8	1248	4 US-09-489-847-101	Sequence 101, App
C 8	9	1.8	1603	3 US-09-009-443-11	Sequence 11, Appli
C 9	9	1.8	1702	3 US-09-413-574-3	Sequence 3, Appli
C 10	9	1.8	1705	4 US-09-205-258-216	Sequence 216, App
C 11	9	1.8	1977	4 US-08-705-477E-99	Sequence 99, Appli
C 12	9	1.8	2073	3 US-09-033-523-6	Sequence 6, Appli

13	9	1.8	2239	4 US-09-581-831-1	Sequence 1, Appli
14	9	1.8	2867	4 US-09-402-532-38	Sequence 38, Appli
C 15	9	1.8	5864	3 US-08-482-918-47	Sequence 47, Appli
C 16	9	1.8	5864	3 US-09-224-681-47	Sequence 47, Appli
C 17	9	1.8	5864	3 US-08-336-728A-47	Sequence 47, Appli
C 18	9	1.8	9278	1 US-08-243-542-9	Sequence 9, Appli
C 19	9	1.8	9278	1 US-08-477-407-9	Sequence 9, Appli
C 20	9	1.8	9278	1 US-08-484-355-9	Sequence 9, Appli
C 21	9	1.8	9646	3 US-08-811-566-1	Sequence 1, Appli
C 22	9	1.8	9646	3 US-09-034-756-1	Sequence 1, Appli
C 23	9	1.8	9704	4 US-09-814-951A-3	Sequence 3, Appli
C 24	9	1.8	11811	3 US-09-078-294-7	Sequence 7, Appli
C 25	9	1.8	12980	3 US-08-811-566-5	Sequence 5, Appli
C 26	9	1.8	12980	4 US-09-034-756-5	Sequence 5, Appli
C 27	9	1.8	23187	4 US-09-499-522-1	Sequence 1, Appli
C 28	9	1.8	35060	3 US-08-814-095-7	Sequence 7, Appli
C 29	9	1.8	42571	4 US-09-810-347-3	Sequence 3, Appli
C 30	9	1.8	55827	4 US-09-813-133A-3	Sequence 3, Appli
C 31	9	1.8	80246	3 US-09-078-294-4	Sequence 4, Appli
C 32	9	1.8	80595	3 US-09-078-294-3	Sequence 3, Appli
C 33	9	1.8	246240	2 US-08-724-394A-20	Sequence 20, Appli
C 34	9	1.8	246240	2 US-08-724-394A-21	Sequence 21, Appli
C 35	9	1.8	246240	2 US-08-724-394A-22	Sequence 22, Appli
C 36	9	1.6	40	3 US-09-306-290-26	Sequence 26, Appli
C 37	8	1.6	54	2 US-08-771-624B-24	Sequence 24, Appli
C 38	8	1.6	144	2 US-08-747-121-2	Sequence 2, Appli
C 39	8	1.6	187	4 US-09-702-705-1474	Sequence 1474, Ap
C 40	8	1.6	187	4 US-09-736-457-1474	Sequence 79, Appli
C 41	8	1.6	247	4 US-09-397-787-79	Sequence 2, Appli
C 42	8	1.6	337	5 PCT-US91-06234A-2	Sequence 2, Appli
C 43	8	1.6	342	4 US-09-056-556-219	Sequence 219, App
C 44	8	1.6	342	4 US-09-072-556-214	Sequence 214, App
C 45	8	1.6	440	4 US-08-579-445-27	Sequence 27, Appli

ALIGNMENTS

RESULT 1

US-09-449-285A-15/c
Sequence 15, Application US/09449285A

Patent No. 6133280

GENERAL INFORMATION:

APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnologie

TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE

FILE REFERENCE: 2676-4232US

CURRENT APPLICATION NUMBER: US/09/449, 285A

CURRENT FILING DATE: 1999-11-24

PRIOR APPLICATION NUMBER: PCT/EP98/03193

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 97201645.5

PRIOR FILING DATE: 1997-06-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15

LENGTH: 555

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: misc_feature

LOCATION: (382)..(555)

OTHER INFORMATION: n can be any nucleotide

US-09-449-285A-15

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

Length: 555

Matches: 10

Conservative: 0

Mismatch: 0

Indels: 0

Gaps: 0

US-09-315-355C-10 (1-501) x US-09-449-285A-15 (1-555)

QY 236 SerLysLeuSerLysLysLysLysLys 245
|||||
31 TCAGAACTCTCAAAAAAAAAAAAAAAAAA 2
DB

RESULT 2
US-09-077-354B-3
; Sequence 3, Application US/09077354B
; Patent No. 6255096
; GENERAL INFORMATION:
; APPLICANT: HOPWOOD, JOHN JOSEPH; SCOTT, HAMISH STEELE;
; APPLICANT: WEBER, BIRGIT, BLANCH, LIANNE; ANSON, DONALD STEWART
; TITLE OF INVENTION: SYNTHETIC MAMMALIAN
; TITLE OF INVENTION: '-N-ACETYLGLUCOSAMINIDASE AND GENETIC SEQUENCES ENCODING SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077.354B
; FILING DATE: 22-APRIL-1999
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00747
; FILING DATE: 22-NOV-1996
; ATTCRENY/AGENT INFORMATION:
; NAME: POKALSKI, ANN R.
; REGISTRATION NUMBER: 34,697
; REFERENCE/DOCKET NUMBER: 12416
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516 742 4343
; TELEFAX: 516 742 4366
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10380 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 17
; FEATURE:
; NAME/KEY: exon 1
; LOCATION: 990..1372
; FEATURE:
; NAME/KEY: exon 2
; LOCATION: 2115..2262
; FEATURE:
; NAME/KEY: exon 3
; LOCATION: 3056..3202
; FEATURE:
; NAME/KEY: exon 4
; LOCATION: 3387..3472
; FEATURE:
; NAME/KEY: exon 5
; LOCATION: 5667..5923
; FEATURE:
; NAME/KEY: exon 6
; LOCATION: 7745..8955
; US-09-077-354B-3

Alignment Scores:
Pred. No.: 17.6 Length: 10380
Score: 10.00 Matches: 10

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.00%
DB: 3
Gaps: 0

US-09-315-355c-10 (1-501) x US-09-077-354B-3 (1-10380)

QY 239 SerLysLysLysLysLysLysLysLysLys 248
|||||
4829 TCAGAACTCTCAAAAAAAAAAGGAGAGAAA 4858
DB

RESULT 3
US-08-520-678A-23/c
; Sequence 23, Application US/08520678A
; Patent No. 5874565
; GENERAL INFORMATION:
; APPLICANT: Rice, Charles M.
; APPLICANT: Kolykhalov, Alexander A.
; TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
; TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520.678A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Henderson, Melodie W.
; REGISTRATION NUMBER: 37,848
; REFERENCE/DOCKET NUMBER: 6029-6836
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; TEXAS:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-520-678A-23

Alignment Scores:
Pred. No.: 5.68 Length: 321
Score: 9.00 Matches: 9
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.80%
DB: 2
Gaps: 0

US-09-315-355c-10 (1-501) x US-08-520-678A-23 (1-321)

QY 240 LysLysLysLysLysLysLysLysLysLys 248
|||||
162 AAAAAAAAAAAAAAAAAAGGAGAGAAA 136
DB

RESULT 4
US-08-897-126-23/c
; Sequence 23, Application US/08897126
; Patent No. 6297003
; GENERAL INFORMATION:

APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Hafeerkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,126
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,678
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-897-126-23
Alignment Scores:
Pred. No.: 5.68 Length: 321
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
Gaps: 0
US-09-315-355C-10 (1-501) x US-08-897-126-23 (1-321)
QY 240 LysLysLysLysLysLysGlyLysLys 248
Db 162 AAAAAAAAAAAAAAAAAAGGAAAAAAA 136
RESULT 5
US-08-520-678A-22/C
Sequence 22, Application US/08520678A
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Hafeerkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,678A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-678A-22
Alignment Scores:
Pred. No.: 6.28 Length: 356
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
Gaps: 0
US-09-315-355C-10 (1-501) x US-08-520-678A-22 (1-356)
QY 240 LysLysLysLysLysLysGlyLysLys 248
Db 216 AAAAAAAAAAAAAAAAAAGGAAAAAAA 190
RESULT 6
US-08-897-126-22/C
Sequence 22, Application US/08897126
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Hafeerkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,126
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,678
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6836
TELECOMMUNICATION INFORMATION:

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TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
TELEX:
:
: INFORMATION FOR SEQ ID NO: 22:
:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 356 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: DNA (genomic)
US-08-897-126-22
:
:
Alignment Scores:
Pred. No.: 6/28      Length: 356
Score: 9/00      Matches: 9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 1.80%      Indels: 0
DB: 3      Gaps: 0
US-09-315-355C-10 (1-501) x US-08-897-126-22 (1-356)
Qy 240 LysLysLysLysLysLysGlyLysLys 248
Db 216 AAAAAAAAAAAAAAAAAAGCAAAAAAAAA 190
:
RESULT 7
US-09-489-847-101
: Sequence 101, Application US/09489847
: Patent No. 6476195
: GENERAL INFORMATION:
: APPLICANT: Rosen et al
: TITLE OF INVENTION: 98 Human Secreted Proteins
: FILE REFERENCE: P2011P1
: CURRENT APPLICATION NUMBER: US/09/489,847
: CURRENT FILING DATE: 2000-01-24
: EARLIER APPLICATION NUMBER: PCT/US99/17130
: EARLIER FILING DATE: 1999-07-29
: EARLIER APPLICATION NUMBER: 60/094,657
: EARLIER FILING DATE: 1998-07-30
: EARLIER APPLICATION NUMBER: 60/095,486
: EARLIER FILING DATE: 1998-08-05
: EARLIER APPLICATION NUMBER: 60/096,319
: EARLIER FILING DATE: 1998-08-12
: EARLIER APPLICATION NUMBER: 60/095,454
: EARLIER FILING DATE: 1998-08-06
: EARLIER APPLICATION NUMBER: 60/095,455
: EARLIER FILING DATE: 1998-08-06
: NUMBER OF SEQ ID NOS: 376
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 101
: LENGTH: 1248
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-489-847-101
:
:
Alignment Scores:
Pred. No.: 21/2      Length: 1248
Score: 9/00      Matches: 9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 1.80%      Indels: 0
DB: 4      Gaps: 0
US-09-315-355C-10 (1-501) x US-09-489-847-101 (1-1248)
Qy 237 LysLysSerLysLysLysLysLysLys 245
Db 1154 AAACTCTCAAAAAAAAAAAAAAAAAA 1180
:
RESULT 8
US-09-007-443-11
: Sequence 11, Application US/09009443

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Patent No. 6259003
GENERAL INFORMATION:
APPLICANT: Fujisawa, Koichi
APPLICANT: Kaekube, Yoshinisa
APPLICANT: Nishiguchi, Susumu
APPLICANT: Maekawa, Yoshiniko
APPLICANT: Allen, Randy Dale
TITLE OF INVENTION: PLANT PROMOTERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 2000 Pennsylvania Avenue, N.W.
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,443
FILING DATE: 20-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mays, Thomas D.
REGISTRATION NUMBER: 34,524
REFERENCE/DOCKET NUMBER: 20455-20113.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/887-1500
TELEFAX: 202/887-0763
INFORMATION FOR SEQ. ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1603 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Gossypium barbadense
TISSUE TYPE: seedling
IMMEDIATE SOURCE:
CLONE: GRC22
US-09-009-443-11

Alignment Scores:
Pred. No.: 27 Length: 1603
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1,80% Indels: 0
DB: 3 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-009-443-11 (1-1603)
QY 241 LyLyLyLyLyLyLyGGLyLyLySser 249
Db 403 AAAAAAAAAAAAAAAAAAGAGT 429

RESULT 9
US-09-413-574-3
Sequence 3, Application US/09413574
Patent No. 6235972
GENERAL INFORMATION:
APPLICANT: Mahajan, Pramod B.
APPLICANT: Taglienti, Laura
TITLE OF INVENTION: Maize Rad33 Gens and Uses Thereof
FILE REFERENCE: 0964
CURRENT APPLICATION NUMBER: US/09/413,574
CURRENT FILING DATE: 1999-10-06
EARLIER APPLICATION NUMBER: 60/109,728
EARLIER FILING DATE: 1998-11-23
NUMBER OF SEQ. ID NOS: 5

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1702
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(1209)
US-09-413-574-3

Alignment Scores:
Pred. No.: 28.7 Length: 1702
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 3 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-413-574-3 (1-1702)
Oy 237 LysleuSerLysLysLysLysLys 245
Db 1670 AAATTATCTAAAAAATAAAAAA 1696

RESULT 10
US-09-205-258-216
; Sequence 216, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007p1
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1281)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1704)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-216

Alignment Scores:
Pred. No.: 28.7 Length: 1705
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 4 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-205-258-216 (1-1705)
Oy 237 LysleuSerLysLysLysLysLys 245
Db 1643 AAATGTCAAAAAATAAAAAA 1669

RESULT 11
US-08-705-477E-99
```

Sequence 99, Application US/08705477E
Patent No. 6569432
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
APPLICANT: Heaton, Warren D.W.
APPLICANT: Fair, William R.
APPLICANT: Overfelli, Quathak
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
FILE REFERENCE: 1769/41426-G
CURRENT APPLICATION NUMBER: US/08/705,477E
CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 99
LENGTH: 1977
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (840)..(843)
OTHER INFORMATION: n=any nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1294)..(1295)
OTHER INFORMATION: n=any nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1338)..(1343)
OTHER INFORMATION: n=any nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1965)..(1966)
OTHER INFORMATION: n=any nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1096)..(1101)
OTHER INFORMATION: n=any nucleotide
US-08-705-477E-99

Alignment Scores:
Pred. No.: 33.1 Length: 1977
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 4 Gaps: 0

US-09-315-355C-10 (1-501) x US-08-705-477E-99 (1-1977)

OY 240 LysLysLysLysLysLysGlyLysLys 248
DB 1786 AAAAAAAAAAAAAAAAAAGCGCAAAAAA 1812

RESULT 1:
US-09-033-523-6
Sequence 6, Application US/09032523
Patent No. 6232454
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl
APPLICANT: Baugh, Mariah
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0479 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2073 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANTCTUT01
CLONE: 1515165
US-09-032-523-6

Alignment Scores:
Pred. No.: 34.7 Length: 2073
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 3 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-032-523-6 (1-2073)

OY 240 LysLysLysLysLysLysGlyLysLys 248
DB 2007 AAAAAAAAAAAAAAAAAAGGAAAAAAG 2033

RESULT 13
US-09-581-831-1
Sequence 1, Application US/09581831
Patent No. 6448020
GENERAL INFORMATION:
APPLICANT: TOFTGARD, RUNE
APPLICANT: ZAPHIROPOULOS, PETER G.
APPLICANT: KOSERMAN, PRIIT
APPLICANT: GRIMM, THOMAS
TITLE OF INVENTION: MOLECULES ASSOCIATED WITH THE HUMAN SUPPRESSOR OF FUSED
FILE REFERENCE: 50695-60568
CURRENT APPLICATION NUMBER: US/09/581,831
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: PCT/SE98/02383
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 9704788-0
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 9802293-2
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2239
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

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; LOCATION: (167)..(1618)
US-09-581-831-1

Alignment Scores:
Pred. No.: 37.4 Length: 2239
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 4 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-581-831-1 (1-2239)

Qy 240 LysLysLysLysLysGlyLysLys 248
Db 2213 AAAAAAAAAAAAAAAAAAGAGAAAAA 2239

RESULT 14
US-09-402-532-38
; Sequence 38, Application US/09402532
; Patent No. 6498019
; GENERAL INFORMATION:
; APPLICANT: Taniyama, Yoshio
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2456USOP
; CURRENT FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: PCT/JP98/01643.
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: JP 10-010289
; EARLIER FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: JP 9-184885
; EARLIER FILING DATE: 1997-07-10
; EARLIER APPLICATION NUMBER: JP 9-093355
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE:
; SEQ ID NO 38
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Unsure (5' flanking promoter sequence of genomic DNA)
US-09-402-532-38

Alignment Scores:
Pred. No.: 47.5 Length: 2867
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 4 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-402-532-38 (1-2867)

Qy 240 LysLysLysLysLysGlyLysLys 248
Db 1316 AAAAAAAAAAAAAAAAAAGAGAAAA 1342

RESULT 15
US-08-482-918-47/c
; Sequence 47, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Sugan, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
```

```
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 5864 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521,
LOCATION: 3932..4088, 4314..4397, 4778..4887, 5208..5275,
LOCATION: 5677..5713)
NAME/KEY: mat_peptide
LOCATION: join(1744..1797, 2693..2755, 3351..3521,
LOCATION: ..4088, 4314..4397, 4778..4887, 5208..5275,
LOCATION: ..5713)
US-08-482-918-47

Alignment Scores:
Pred. No.: 95.2 Length: 5864
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 3 Gaps: 0

US-09-315-355C-10 (1-501) x US-08-482-918-47 (1-5864)

Qy 240 LysLysLysLysLysGlyLysLys 248
Db 5792 AAAAAAAAAAGAGAGAGAGAG 5766
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Search completed: January 31, 2004, 04:45:08
Job time : 93 secs

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Score: 395.00 Matches: 395
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.84% Indels: 0
DB: 12 Gaps: 0

US-09-315-355c-10 (1-501) x US-10-264-049-376 (1-2584)

107 AspaIaGIuThrLeuGIuSerLeuLeuGIuLeuThraValIYrGIySerAsnAspGln 126
131 GATCTGAGACTCTTGGAATCTCTCTGGGCTTACGCTTACGGAGAGTAATCA 190
127 AspProIYrValThrLeuYAspThrGIuInIYrGIuArgGIuAspPheLeuIlys 146
191 GATCTTACGTTACTCTGAAGATACAGAACATATGAACCTGAAGATTCTTGATTAAG 250
147 ProSerAspLeuLeuIleValCYeGIyArgIaGIuInAspGlnCYeAsnLeuGIuVal 166
251 CCCAGTGAATATCTTATGTTGTGGCCGACCTGAACGAGCCAGTGCATTTAGAGGTG 310
167 HisValIYrAsnGIuGIuAspSerPheThYrValHisHisAspIleLeuLeuSerAla 186
311 CATGTTTATATCAAGAAAGAGACTTTTATGACCAATGATATATCTTGTCTGCA 370
187 TyrProLeuSerValGIuTrpLeuAsnPheAspProSerProAspAspSerThrGIyAsn 206
371 TATCCTCTGAGTGGATGGCTGATTTGATCTTACCCAGATGATTTACTGGAAT 430
207 TyrIleAlaValGIyAsnMetThProValIleGIuValITrPAspLeuAspIleValAsp 226
431 TACATTGCTGTAGGAAACATGACCCCTGTTATGAGGTGGACCTTGATATAGTGAC 490
227 SerLeuGIuProValPheThrLeuGIySerIysLeuSerIysIysIysValYsGIy 246
491 TCTTACGCAAGTCTTACACTCGAGCTAACTTTTAAAGAAAGAAAGAAAGCA 550
247 LysIysSerSerSerSerAlaGIuGIyHisThrAspAlaValLeuAspLeuSerITrPAsnIys 266
551 AAGAAGAGTCTCTGACGAAAGGGGATACCGATGCTGCTTGAACCTTCAATGGAATAG 610
267 LeuIleAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuITrPAspMet 286
611 CTAATCAGAAATGTTTGAAGAGTGCATGACGACACACAGTGAATCTGTGGATATAG 670
287 SerLeuGIyLysProAlaAlaSerLeuAlaValHisThrAspIysValGIuThrLeuGln 306
671 TCCCTGGGAAACCGACAGCTAGCCTCGCTGACACAGACAGAGTCCAAACACTGAG 730
307 PheHisProPheGIuAlaGlnThrLeuIleSerGIySerITrAspIysSerValAlaLeu 326
731 TTTTATCATTTTGAAGCAGACACTCTGATTTCTGCTCATATGATTAAGTGTGCTTGG 790
327 TyrAspCYeArgSerProAspGlnSerHisArgMetITrPAspPheSerGIyGlnIleGIu 346
791 TATGCTGCCAAGTCCAGATGAAGCCATGCAATGTGGCATTCAGTGGCAGATAGAG 850
347 ArgValITrPAsnHisPheSerProCYeHisPheLeuAlaSerThrAspAspGIyPhe 366
851 AGAGTGACTTGAATCAGCTTTTCACTTGTGATTTCTTGGCCAGTACAGATGACGGCTTT 910
367 ValITrAsnLeuAspAlaArgSerAspIysProIlePheITrLeuAsnAlaHisAsnAsp 386
911 GTATATATTTTGAATGACGTTTACATTAAGCCAAATTTTACCTTAATGACACATATAT 970
387 GluIleSerGIyLeuAspLeuSerSerGlnIleYsGIyCYeLeuValThrAlaSerAla 406
971 GAAATCTGCTGCTTGAATCTTACAGTCAATCAAGGCTGCTGTGATGCTTCACTCACT 1030
407 AspIysITrValIysIleITrPAspIleLeuGIyAspArgProSerLeuValHisSerArg 426
1031 GACAAATACGTGAAGATCTGGACATCTTAGAGATAGCCAAAGTCTGATTCATTTAGG 1090
427 AspMetIysMetGIyValLeuPheCYeSerSerCYeSProAspLeuProPheIleITyr 446

1091 GACATGAAATGGAGAGTCTCTTCTGTTCTCAATGTCCTGATTTGCCATTTATTTAT 1150
447 AlAPheGIyGIyGIuInYsGIuGIyLeuArgValITrAspIleSerThrValSerSerVal 466
1151 GCCTTTGGAGGTCAAAAGAGGCTTCCGGCTTGGATATTAAGCAGACTCTTTCAGTA 1210
467 AsnGIuAlaPheGIyArgArgGIuArgLeuValLeuGIySerAlaArgAsnSerSerIle 486
1211 AATGAACATTTTGAAGACGAGAGGCTTGTCTTGGAGTGCAGAAATTCATTTAT 1270
487 SerGIyProPheGIySerArgSerSerAspThrProMetGlnSer 501
1271 AGTGGCCCTTTTGGCAGACAGAGCTCAGATACACCCATGAGGCT 1315

RESULT 2

US-10-012-697-1445
Sequence 1445, Application US/10012697
Publication No. US20030215803A1
GENERAL INFORMATION:
APPLICANT: Escobedo, Jaime
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Kassem, Alfat
APPLICANT: Lamson, George
APPLICANT: Scott, Beth
APPLICANT: Drmanac, Radoje
APPLICANT: Crkenjakov, Radomir
APPLICANT: Dickson, Mark
APPLICANT: Drmanac, Snezana
APPLICANT: Labat, Ivan
APPLICANT: Leshkowitz, Dena
APPLICANT: Kila, David
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Steche-Crain, Birgit
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OR INVENTION: ISOLATED FROM HUMAN PROSTATE
FILE REFERENCE: 2300-16252
CURRENT APPLICATION NUMBER: US/10/012,697
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/275,668
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1445
LENGTH: 1468
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-697-1445

Alignment Scores:

Pred. No.: 1,55e-242 Length: 1468
Score: 253.00 Matches: 253
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.50% Indels: 0
DB: 13 Gaps: 0

US-09-315-355c-10 (1-501) x US-10-012-697-1445 (1-1468)

249 SerSerSerIaGIuGIyHisThrAspAlaValLeuAspLeuSerITrPAsnIysLeuIle 268
707 AGTTCCTCAGAGAGGAGCAATCCGATGCTGTCTTACCTTATGAAATAGCTAATC 766
269 ArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuITrPAspMetSerLeu 288
767 AGAATGTTTGAAGAAATGATCAGTGCAGACACCTGTAATTCGTGGATATATCTCTTG 826
289 GIyLysProAlaAlaSerLeuAlaValHisThrAspIysValGlnThrLeuGlnPheHis 308
827 GGAAGAACGAGAGCTAGCTCTGCTGTACACAGACAGCAAGGTCCAAACACTGCACTTTCAT 886

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QY 309 ProhEgLuAgiNthrlEueIleSergIlySerTyraSplySerValAlaLeuTyraSp 328
Db 887 CCATTGAGACAGACCTGATTTCTGGCTCATATGATAGTCAGTGGCTTTGATGAC 946
QY 329 CyarGerProAppluSerHisArgMetTrpArgPheSerGlyGlnIleGluArgVal 348
Db 947 TGCAGAGTCCAGATGGAAGCCATGCAATGTGGGCAATTCAGTGGCAGATGAGAGATG 1006
QY 349 ThrTrpAsnHisPheSerProCyHisPheLeuAlaSerThrAspAspGlyPheValTyr 368
Db 1007 ACTTGAAATCACTTTTCACTTGTCATTTCTTGCCAGTACAGATGACGGCTTTGATAT 1066
QY 369 AsnLeuAspAlaArgSerAspSlyProIlePheThrLeuAsnAlaHisAsnAspGluIle 388
Db 1067 AATTGGATGACCTTGACATGCAATGCCAATTTTACACTTATGACACACAAATGAAATC 1126
QY 389 SerGlyLeuAspLeuSerSerGlnIleGlyGlyCysLeuValThrAlaSerAlaAspIys 408
Db 1127 TCTGTCTTGATCTTACAGATCAATCAAGGCTGTCTCGACTGCTTCAGTGCAGACAA 1186
QY 409 TyrAlaIysIleTpaPbIleLeuGlyAspArgProSerLeuValHisSerArgAspMet 428
Db 1187 TACGTGAAGATCTGGACATCTTAGAGATAGGCCAAGCTAGATTCATTAGAGGACATG 1246
QY 429 LysMetGlyValLeuPheCysSerSerCysCysProAspLeuProPheIleTyrAlaPhe 448
Db 1247 AAAATGGAGATCTCTCTGCTCTTCAATGTTGCCCTGATTTGCCATTTATTAAGCTTT 1306
QY 449 GlyGlyGlnIysGluGlyLeuArgValTrpAspIleSerThrValSerSerValAsnGlu 468
Db 1307 GGAAGTCAGAAAAGAGGCTTCGGGCTCGGATATTAAGCACAGCTCTTCACTAAATGAA 1366
QY 469 AlaPheGlyArgArgGluArgLeuValLeuGlySerAlaArgAsnSerIleSerGly 488
Db 1367 GCATTGTGAACAGACAGAGGCTTGTCTTGGAGTGCAGAAATTCATTTATTAAGTGC 1426
QY 489 ProhEgLySerArgSerSerAspThrProMetGlySer 501
Db 1427 CCTTTTGGCAGCAGAGCTCAGATACACCCATGAGTCT 1465

RESULT 3
US-10-242-535A-9829
; Sequence 9829, Application US/10242535A
; Publication No. US2004001363A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9829
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (38)..(38)
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; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-9829
Alignment Scores:
Pred. No.: 2 66e-93 Length: 400
Score: 103.00 Matches: 103
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.56% Indels: 0
DB: 12 Gaps: 0

US-09-315-355C-10 (1-501) x US-10-242-535A-9829 (1-400)
QY 399 GlyCysLeuValThrAlaSerAlaAspIysTyrValIysIleTrpAspIleLeuGlyAsp 418
Db 76 GCGCTGTCTCGATGCTGCTTACGCTGACCAATAGCAATCTGGACATCTTGAAGAT 135
QY 419 ArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCysSerSerCys 438
Db 136 AGGCCAAGTCTAGTTCATTCTAGGACATGAAATGGAGTTCCTCTGTTCTTCATGT 195
QY 439 CysProAspLeuProPheIleTyrAlaPheGlyGlyGlnIysGluGlyLeuArgValTrp 458
Db 196 TGCCCTATTTGCCATTTATTTATGCTTTGGAGCTCAAAAAGAGGCTTTGGGCTTGG 255
QY 459 AspIleSerThrValSerSerValAsnGluAlaPheGlyArgArgGluArgLeuValLeu 478
Db 256 GATTAAGCACAGCTCTTCTTCAATGAATGAAGCATTTGGAAGACAGAGAGCTTGTCTT 315
QY 479 GlySerAlaArgAsnSerSerIleSerGlyProhEgLySerArgSerAspThrPro 498
Db 316 GGGAGTCAGAAATTCATCATTAATAGTGCCCTTTTGGCAGCAGAGACTCAGATACACC 375
QY 499 MetGlySer 501
Db 376 ATGAGTCT 384

RESULT 4
US-10-242-535A-16383
; Sequence 16383, Application US/10242535A
; Publication No. US2004001363A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16383
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-16383
Alignment Scores:
Pred. No.: 3 35e-72 Length: 568
Score: 82.00 Matches: 82
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.37% Indels: 0
DB: 12 Gaps: 0

US-09-315-355C-10 (1-501) x US-10-242-535A-16383 (1-568)
```

QY 302 ValGlnThrIleuGlnPheHisProPheGluAlaGlnThrIleuIleSerGlySerTyrAsp 321
Db 171 GTCGAACACCTGCAGCTTTCATCCATTTGACACAGACTCGATTTCGGCTCATATGAT 230
QY 322 LysSerValAlaLeuTyrAspCysArgSerProAspGluSerHisArgMetTyrAspPhe 341
Db 231 AAGTCAGTGGCTTTGATGATGATGCGGAAGTCAGATGAAACCCATGCAATGTGGCGGATTC 290
QY 342 SerGlyGlnIleGluArgValThrTyrAsnHisPheSerProCysHisPheLeuAlaSer 361
Db 291 AGTGGCGAGATGAGAGAGTACTGGAATACCTTTCACCTTGTCATTTCCTGGCCAGT 350
QY 362 ThrAspAspGlyPheValTyrAsnLeuAspAlaArgSerAspLysProIlePheThrIleu 381
Db 351 ACAATGACGGCTTTGATATATTAATTTGATGATGATGATGATGATGATGATGATGATGAT 410
QY 382 AsnAla 383
Db 411 AATGCC 416

RESULT 5

US-09-915-995-21467
; Sequence 21467, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 21467
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ... (508)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-21467

Alignment Scores:

Pred. No.: 2,92e-62 Length: 508
Score: 72.00 Matches: 72
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.37% Indels: 0
DB: 11 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-918-995-21467 (1-508)

QY 430 MetGlyValLeuPheCysSerSerCysCysProAspLeuProPheIleTyrAlaPheGly 449
Db 61 ATGGAGATTCCTCTTCTTCTTCAAGTGGCCCTGATTTGCAATTAATTAATGATGATGATGAT 120
QY 450 GlyGlnIleGluGlnIleuArgValTyrAspIleSerThrValIleSerSerValAsnGluAla 469
Db 121 GGTCAAAAGAGAGAGGCTTGGGCTGCGATTAAGCAAGCTCTTCAAGTAAAGAGCA 180
QY 470 PheGlyArgArgGluArgLeuValIleuGlySerAlaArgAsnSerSerIleSerGlyPro 489
Db 181 TTGGAAGACAGAGAGGCTTGTCTTGGGAGTGCACAAATTCATTAATGAGCCCT 240
QY 490 PheGlySerArgSerSerAspThrProMetGluSer 501
Db 241 TTGGCAGCAGAGAGCTCAGATACCCCATGAGATCT 276

RESULT 6

US-10-062-674-1561
; Sequence 1561, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062, 674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1561
; LENGTH: 3024
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 124921.6
; NAME/KEY: unsure
; LOCATION: (1) ... (3024)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-1561

Alignment Scores:

Pred. No.: 1,44e-60 Length: 3024
Score: 71.00 Matches: 97
Percent Similarity: 97.98% Conservative: 0
Best Local Similarity: 97.98% Mismatches: 0
Query Match: 14.17% Indels: 2
DB: 12 Gaps: 0

US-09-315-355C-10 (1-501) x US-10-062-674-1561 (1-3024)

QY 337 ArgMetTyrArgPheSerGlyGlnIleGluArgValThrTyrAsnHisPheSerProCys 356
Db 1211 CGAATGGCGGATTCAGTGGCGAGATGAGAGAGTGCATTTGCAATCACTTTGACCTTGT 1270
QY 357 HisPheLeuAlaSerThrAspAsp-GlyPheValTyrAsnLeuAspAlaArgSerAspLys 376
Db 1271 CATTCTTGGCCAGTACAGATGAGAGGCGCTTGTATTAATTTGATGACAGCTTCAGATAA 1330
QY 376 sProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSerGly 396
Db 1331 GCCAATTTTACACTTATATGACACAAATGATGAAATCTCGCTTATGATGATGATGATGAT 1390
QY 396 nIle-IysGlyCysLeuValThrAlaSerAlaAspLysTyrValIleTyrAspIleL 416
Db 1391 AATCCAAAGGCGCTGCTGTCGATGACCTTCACTGACCAAAATGATGAGATCTGGAGACATCT 1450
QY 416 euGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeu 433
Db 1451 TAGGAGATAGGCCAAGCTGATTCATTTAGGAGACATGAAAATGGAGTTCTC 1503

RESULT 7

US-10-029-386-9515
; Sequence 9515, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9515
; LENGTH: 539

```

? TYPE: DNA
? ORGANISM: Homo sapiens
FEATURE:
? OTHER INFORMATION: MAP TO CHR12.3
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89
? OTHER INFORMATION: EST HUMAN HIT: AW60781.1, EVALUATE 1.00e-10
? OTHER INFORMATION: SWISSPROT HIT: Q13610, EVALUATE 4.00e-04
? OTHER INFORMATION: NT HIT: g114766316, EVALUATE 1.00e-101
NS-10-029-386-9515
```

Pred. No.:	2,96e-52	Length:	538
Score:	62.00	Matches:	62
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12.38%	Indels:	0
DB:	13	Gaps:	0

US-09-315-355C-10 (1-501) x US-10-029-386-9515 (1-539)

Qy 45 G|u|g|u|g|y|c|y|g|y|s|e|r|a|s|p|g|u|g|u|g|u|u|t|t|t|g|y|s|e|r|p|r|o|s|e|r|g|u|a|s|p|g|y|m|e|t|s|l|n 64
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 Db 284 G|A|G|A|G|G|T|G|C|A|G|T|G|A|T|G|A|A|G|G|A|G|G|A|C|A|G|G|C|A|G|T|C|T|T|C|A|G|A|G|A|G|A|T|G|C|A|T|G|C|A|G 343

Dy 65 SerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAspAsp 84
Dd 344 AGTGCACGCCACCGAGCAGCCCMAGAGAGCCCTGGAGGATGTGACCCAGAGATGAC 403

Qy 85 ArgHrLeuSpaSpaSpGluLeuAglIuYrAspLeuAspLysTyRAspGluGluIly 104
 |||||
 Db 404 AGAGCGCTTGATGATGATGAGCTGCGCTGAGTACGACTTAGAATAATGATGAGGAGGT 463

QY	105	AspPro	106
Db	464	GACCCA	469

RESULT 8

US-10-029-386-23215
; Sequence 23215, Application US/10029386
; Publication No. US20030194704A1
GENERAL INFORMATION

: APPLICANT: Penn, Sharon G.
 : APPLICANT: Rank, David R.
 : APPLICANT: Hanzel, David K.
 : TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
 : TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
 : FILE REFERENCE: A60MICA-X-2

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;
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23215
;

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TYPE: DNA

FEATURE:

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89

OTHER INFORMATION: NT HIT: g114766316, EVALUE 1.00e-85

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; OTHER INFORMATION: SWISSPROT HIT: Q13610, EVALUUE 9.00e-11
HS-10-029-386-23215

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Alignment Scores:

Pred. No.:	9.66e-44	Length:	161
Score:	53.00	Matches:	53
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	10.58%	Indels:	0
DB:	13	Gaps:	0

US-09-315-355C-10 (1-501) X US-10-029-386-23215 (1-161)

Qy 48 GlyGlySeraspGluGluGluThrGlySerProSerGluaspGlyMetGlnSerAlaArg 67
Db 1 GGTGCAGTATGAAAGAGAGACAGGCAGTCCCTTCAGAAAGATGCATGCAGAGTGCACGC 60

Qy 68 ThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAspAspArgThrLeu 87
Db 61 ACCACGACGCGCCACAGAGAGCCCTCGAGGATGTGACCCAGAGATGACAGACGCTT 120

QY 88 ASPASPSPGLULEVALAGLUTYRRASPLEUASPLSYTYR 100
DB 121 GATGATGATGAGCTGGCTGAGTACGACTTAGATAAATAT 159

RESULT 9

US-09-880-107-2725/c
; Sequence 2725, Application US/09880107
; Patent No. US20020142981A1
; Inventor: TUDORCOT

```

; GENERAL INFORMATION:
;
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G
;

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; APPLICANT: Schert, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; PCT NUMBER: 01/001500

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; CURRENT APPLICATION NUMBER: US/09/880,107
 ;
 ; CURRENT FILING DATE: 2001-06-14
 ;
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ;
 ; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: DataWarrior 3.1

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; SEQ ID NO 2725
;
; LENGTH: 150
; TYPE: DNA
;

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FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020142981A1 N92948
US-09-880-107-2725

Pred. No.:	8,93e-40	Length:	150
Score:	49.00	Matches:	49
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.78%	Indels:	0
DB:	10	Gaps:	0

US-09-315-35EC-10 (1-501) x US-09-880-107-2725 (1-150)
Qy 192 GluTrpLeuAsnPhaAspProSerBroAspAsSerThro

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RESULT 10

US-10-062-674-1082
: Sequence 1082 A

```

; Publication No. US2004000559A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Ioring, Jeanne F.; Kaser, Matthew R.
;
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
;
; FILE REFERENCE: PA-0026-1 CIP
;
; CURRENT APPLICATION NUMBER: US/10/062,674
;
; CURRENT FILING DATE: 2002-01-30

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;; PRIOR APPLICATION NUMBER: US 09/625,102
;; PRIOR FILING DATE: 2000-07-24
;; NUMBER OF SEQ ID NOS: 2217
;; SOFTWARE: PERL Program
;; SEQ ID NO 1082
;; LENGTH: 313
;; TYPE: DNA
;; ORGANISM: Mus musculus
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: GenBank ID No. US2004005559A1 91677315
US-10-062-674-1082

Alignment Scores:
Pred. No.: 1,71e-36 Length: 313
Score: 46.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.18% Indels: 0
DB: Gaps: 0

US-09-315-355c-10 (1-501) x US-10-062-674-1082 (1-313)

Qy 221 Aspleuasp11eValaspSerLeuGluProValpHeThLeuGlySerLyLeuSerLyS 240
Db 3 GACCTGATATAGTGAAGCTCTCTGAAACCACTCTTCACTGGAGCAAGCTTCCAAA 62

Qy 241 LybalySlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySly 260
Db 63 AAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 122

Qy 261 AspleuSerTPanLyS 266
Db 123 GACCTATCTCGAATTAAG 140

RESULT 11.
US-10-012-697-413/C
;; Sequence 413, Application US/10012697
;; Publication No. US20030215803A1
;; GENERAL INFORMATION:
;; APPLICANT: Escobedo, Jaime
;; APPLICANT: Garcia, Pablo Dominguez
;; APPLICANT: Kassam, Altaf
;; APPLICANT: Lamson, George
;; APPLICANT: Scott, Beth
;; APPLICANT: Drmanac, Radoje
;; APPLICANT: Cirvenjakov, Radomir
;; APPLICANT: Dickson, Mark
;; APPLICANT: Drmanac, Snezana
;; APPLICANT: Labat, Ivan
;; APPLICANT: Leeshkowitz, Dena
;; APPLICANT: Kita, David
;; APPLICANT: Garcia, Veronica
;; APPLICANT: Jones, Lee William
;; APPLICANT: Steche-Crain, Birgit
;; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
;; TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
;; FILE REFERENCE: 2300-16252
;; CURRENT APPLICATION NUMBER: US/10/012,697
;; CURRENT FILING DATE: 2003-01-21
;; PRIOR APPLICATION NUMBER: 60/254,648
;; PRIOR FILING DATE: 2000-12-07
;; PRIOR APPLICATION NUMBER: 60/275,668
;; PRIOR FILING DATE: 2001-03-13
;; NUMBER OF SEQ ID NOS: 1568
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 413
;; LENGTH: 667
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 3, 10, 12, 434, 452, 457, 575, 589, 611, 615, 633, 640,
;; NAME/KEY: misc feature
```

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;; LOCATION: 663
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 3, 10, 12, 434, 452, 457, 575, 589, 611, 615, 633, 640,
;; LOCATION: 663
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 3, 10, 12, 434, 452, 457, 575, 589, 611, 615, 633, 640,
;; LOCATION: 663
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 3, 10, 12, 434, 452, 457, 575, 589, 611, 615, 633, 640,
;; LOCATION: 663
;; OTHER INFORMATION: n = A,T,C or G
US-10-012-697-413

Alignment Scores:
Pred. No.: 3.27e-29 Length: 667
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.78% Indels: 0
DB: Gaps: 0

US-09-315-355c-10 (1-501) x US-10-012-697-413 (1-667)

Qy 168 ValTyRanGlnGlnGluGluAspSerPheTyRValHisAspPleLeuSerAlaTyR 187
Db 244 GTTATATATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 185

Qy 188 ProLeuSerValGluTrpLeuAsnPheAspProSerProAspAspSerThrgLyAsn 206
Db 184 CCTGTAGTGTGGAATGGCTGAAATTTTGATCTAGCCAGATATATCTACTGTAAT 128

RESULT 12.
US-10-242-535A-57161
;; Sequence 57161, Application US/10242535A
;; Publication No. US20040013663A1
;; GENERAL INFORMATION:
;; APPLICANT: ChondroGene Inc.
;; APPLICANT: Lew, C.C.
;; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
;; FILE REFERENCE: 4231/2005
;; CURRENT APPLICATION NUMBER: US/10/242,535A
;; CURRENT FILING DATE: 2002-09-12
;; PRIOR APPLICATION NUMBER: US 10/085,783
;; PRIOR FILING DATE: 2002-02-28
;; PRIOR APPLICATION NUMBER: US 60/305,340
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/275,017
;; PRIOR FILING DATE: 2001-03-12
;; PRIOR APPLICATION NUMBER: US 60/271,955
;; PRIOR FILING DATE: 2001-02-28
;; NUMBER OF SEQ ID NOS: 58994
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 57161
;; LENGTH: 222
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (24)-(24)
;; OTHER INFORMATION: n is a, c, g, or t
;; FEATURE:
;; NAME/KEY: misc feature
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US-09-315-355C-10 (1-501) x US-10-027-632-144482 (1-686)

US-09-315-355C-10 (1-501) x US-10-242-535A-57161 (1-222)

US-10-027-632-144482/c
Sequence 144482, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 144482
LENGTH: 686
TYPE: DNA
ORGANISM: Human
US-10-027-632-144482

Alignment Scores:
Pred. No.: 1,17e-19 Length: 222
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.79% Indels: 0
DB: 12 Gaps: 0

US-09-315-355C-10 (1-501) x US-10-242-535A-57161 (1-222)

OY 69 GHAlAARgProARgGluProLeuGIuAspGIyAspProGIuAspAspArgThrLeuAsp 88
Db 62 CAGGCGACGCCCAAGAGAGGCCCGCCCGAGATGTGACCCAGAGATGACAGAGACGCTTGAT 122
OY 89 AspspGluLeuAlaGluIyTrAspLeu 97
Db 122 GATGATGAGCTGGCTGAGTACACTTA 148

RESULT 13
US-10-027-632-144482/c
Sequence 144482, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 144482
LENGTH: 686
TYPE: DNA
ORGANISM: Human
US-10-027-632-144482

Alignment Scores:
Pred. No.: 3.17e-15 Length: 686
Score: 25.00 Matches: 25
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.99% Indels: 0
DB: 13 Gaps: 0

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QY      1 MetAsnArSerzrgInValThrCysValAlaTrpValArgCysGlyValAlaIysGlu 20
Db      130 ATGAACCGCAGCCGCCAGGTGACGTGCTGGGTCCGCTGCGCGTGGCCAAAGAG 71
      21 ThrProAspIysVal 25
      |||||
Db      70 ACACCGACAGCAAGGTG 56

RESULT 14
US-10-027-632-144482/c
; Sequence 144482, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108627.129
; CURRENT FILING DATE: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144482
; LENGTH: 686
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-144482

Alignment Scores:
Pred. No.:          3,17e-15          Length:          686
Score:              25.00             Matches:          25
Percent Similarity: 100.00%           Conservative:    0
Best Local Similarity: 100.00%         Mismatches:     0
Query Match:        4.99%             Indels:          0
DB:                 14                Gaps:            0

US-09-315-355C-10 (1-501) x US-10-027-632-144482 (1-686)
QY      1 MetAsnArSerzrgInValThrCysValAlaTrpValArgCysGlyValAlaIysGlu 20
Db      130 ATGAACCGCAGCCGCCAGGTGACGTGCTGGGTCCGCTGCGCGTGGCCAAAGAG 71
QY      21 ThrProAspIysVal 25
      |||||
Db      70 ACACCGACAGCAAGGTG 56

RESULT 15
US-09-998-598-1166/c
; Sequence 1168, Application US/0998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606

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; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO: 1168
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-1168
    
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Alignment Scores:
Pred. No.:      0.0217      Length:      476
Score:          12.00      Matches:      12
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      2.40%      Indels:      0
DB:               10      Gaps:      0
    
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US-09-315-355c-10 (1-501) x US-09-998-598-1168 (1-476)

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QY      240  LysLysLysLysLysLysGlyLysLysSerSerSer 251
           |||||
Db       75  AAAAAAAAAAAAAAAAAAGGAAAAAAAAAGCAGCTCT 40
    
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Search completed: January 31, 2004, 06:02:16
 Job time : 510 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

Run on: January 31, 2004, 03:57:49 ; Search time 489 Seconds

(without alignments)
3733.994 Million cell updates/sec

Title: US-09-315-355C-10

Perfect score: 2640

Sequence: 1 MNRSRQVTCAWVRGVAKE.....RNSISGPGFGRSSDTPMES 501

Scoring table:

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Xgapop 6.0			
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Searched: 2434939 segs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -OFMT=fastab -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=Blosum62
-TRANS=numa40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09315355 @CGN 1.1.85 @runat_30012004_091907_24434
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-LONLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2:	/cgn2_6/ptodata/2/pubpna/PTCT_NEW_PUB.seq.*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8:	/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16:	/cgn2_6/ptodata/2/pubpna/US10D_NEW_PUB.seq.*
17:	/cgn2_6/ptodata/2/pubpna/US10E_NEW_PUB.seq.*
18:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	2547.5	96.5	1468	13	US-10-012-697-1445	Sequence 1445, Ap
2	2084	78.9	2584	12	US-10-264-049-376	Sequence 376, App
3	1759.5	66.6	3024	12	US-10-062-674-1561	Sequence 1561, Ap
4	935.5	35.4	1620	15	US-10-128-714-2208	Sequence 2208, Ap
5	929.5	35.2	1629	15	US-10-128-714-7208	Sequence 7208, Ap
6	908.5	34.4	1697	15	US-10-128-714-6208	Sequence 6208, Ap
7	908.5	34.4	1617	15	US-10-128-714-2208	Sequence 208, App
8	908.5	34.4	1617	15	US-10-128-714-5208	Sequence 5208, App
9	907.5	34.4	1617	15	US-10-128-714-1208	Sequence 1208, App
10	826	31.3	1839	13	US-09-949-029-59	Sequence 59, App1
11	743.5	28.2	1638	13	US-10-032-585-6502	Sequence 6502, Ap
12	733.5	27.8	1638	13	US-10-320-797-2234	Sequence 2234, Ap
13	708	26.8	1918	12	US-10-320-797-1234	Sequence 1234, Ap
14	708	26.8	3292	12	US-10-320-797-234	Sequence 234, App
15	588.5	22.3	2895	12	US-09-938-842A-2540	Sequence 2540, Ap
16	588.5	22.3	2895	12	US-09-938-842A-16383	Sequence 16383, A
17	578	21.9	568	12	US-10-242-535A-15383	Sequence 15383, A
18	545	20.6	400	12	US-10-242-535A-9829	Sequence 9829, Ap
19	473	17.9	313	12	US-10-062-674-1082	Sequence 1082, Ap
20	408	15.0	508	11	US-09-918-995-21467	Sequence 21467, A
21	397	15.0	539	13	US-10-029-386-9515	Sequence 9515, App
22	344.5	13.0	519	11	US-09-770-961-49	Sequence 49, App1
23	342	13.0	222	12	US-10-242-535A-57161	Sequence 57161, A
24	282	10.7	161	13	US-10-029-386-23215	Sequence 23215, A
25	262	9.9	150	10	US-09-880-107-2785	Sequence 2785, App
26	251	9.5	1830	12	US-10-369-493-43872	Sequence 43872, A
27	235.5	8.9	3015	12	US-10-369-493-43929	Sequence 43929, A
28	233	8.8	840	12	US-10-369-493-43586	Sequence 43586, A
29	226	8.6	1446	12	US-10-369-493-25975	Sequence 25975, A
30	220.5	8.4	1434	12	US-10-369-493-42592	Sequence 42592, A
31	217.5	8.2	1275	10	US-09-938-842A-299	Sequence 299, App
32	217.5	8.2	1275	12	US-09-938-842A-299	Sequence 299, App
33	216.5	8.2	3358	12	US-10-369-493-42532	Sequence 42532, A
34	216.5	8.2	3420	12	US-10-369-493-42740	Sequence 42740, A
35	216	8.2	667	13	US-10-012-697-413	Sequence 413, App
36	216	8.2	2280	11	US-09-893-519A-98	Sequence 98, App1
37	216	8.2	4206	15	US-10-198-846-9917	Sequence 9917, App
38	216	8.2	4207	12	US-10-264-049-614	Sequence 614, App
39	216	8.2	4299	9	US-09-925-301-155	Sequence 155, App
40	216	8.2	4601	15	US-10-106-638-1642	Sequence 1642, App
41	212	8.0	1016	12	US-10-260-298-504	Sequence 504, App
42	209	7.9	1818	12	US-10-369-493-42594	Sequence 42594, A
43	208.5	7.9	1248	10	US-10-369-493-27695	Sequence 27695, A
44	207	7.8	1248	12	US-09-938-842A-298	Sequence 298, App
45	207	7.8	1248	12	US-09-938-842A-298	Sequence 298, App

ALIGNMENTS

RESULT 1
US-10-012-697-1445
; Sequence 1445, Application US/10012697
; Publication No. US20030215803A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Kassam, Altat
; APPLICANT: Kassam, George
; APPLICANT: Scott, Beth
; APPLICANT: Drmanac, Radoje
; APPLICANT: Cirkenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
; TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
; FILE REFERENCE: 2300-16252
; CURRENT APPLICATION NUMBER: US/10/012,697

; CURRENT FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: 60/254,648
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: 60/275,668
 ; PRIOR FILING DATE: 2001-03-13
 ; NUMBER OF SEQ ID NOS: 1568
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1445
 ; LENGTH: 1468
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-012-697-1445

Alignment Scores:
 Pred. No.: 2,28-297 Length: 1468
 Score: 2547.50 Matches: 488
 Percent Similarity: 97.21% Conservative: 0
 Best Local Similarity: 97.21% Mismatches: 0
 Query Match: 96.50% Indels: 14
 DB: 13 Gaps: 1

US-09-315-355c-10 (1-501) x US-10-012-697-1445 (1-1468)

QY 1 MetasnaargseraglnvalthrCysvalalatrpyalargCysgilyvalalalyglu 20
 Db 1 ATGAACCGCAGCCGCCAGGTGACGTGGCGCTGGCGCTGCCGCTGGCCCAAGAG 60
 QY 21 ThrproaplysvaialgluSerlygluVallylsargleuilealaglualys 40
 Db 61 ACACCAAGCAAGTAGAGCTGATGAAGAAGATAAACCCTCATTCCTGAGGCAAG 120
 QY 41 GluylsleuglgluylgllygllySeraspgluylgluThrlyserProserglu 60
 Db 121 GAGAAATTCGCAAGAAAGGTGGTGGCAGTGTGAAGAGGAGCAGCAAGCTTCAGAA 180
 QY 61 AspqlymecglinseralaaargthrlalaaargProarglupoleugluaspGlyasp 80
 Db 181 GATGCGATGCGAGATGCGACGCCAGCCCAAGAGAGCCCTGGAGAGTGTGAC 240
 QY 81 Progluapaspagthrluaspaspaspaspaspaspaspaspaspaspaspaspasp 100
 Db 241 CCAAGAGATGACAGAGCTTGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 101 AspqluylgluylaspProaspalagluthrleuglygluSerleuLeuGlyLeuThrVal 120
 Db 301 GATAGAGAGGTGACCCAGATGCTGAGACTCTTGTAATCTCTTGCGGTCTTACGCTC 360
 QY 121 TyrglyserasnaaspGlnaspProtyrvalThrleuylsaspThrlygluThrlyarg 140
 Db 361 TACGGAGTATGATCAAGATCTTACGTACTCGAAGATACAGAACAATATGAACT 420
 QY 141 GluaspheleuilelyrProserAspaspaspaspaspaspaspaspaspaspaspasp 160
 Db 421 GAAATATTCCTGATTAAGCCAGATGATTAATTAATTAATTAATTAATTAATTAATTA 480
 QY 161 GlnCysasnaeuGlualHisvallyrAsnaglgluaspserPheTyrrValHis 180
 Db 481 CAGTGCATTTAGAGCTGCATTTATTAATCAAGAAGACTTTTATTAATCAACAT 540
 QY 181 AspilleuLeuSeraillyrProleuSerValgluThrleuaspPheaspProserPro 200
 Db 541 GATATACCTCTGCTGCATATCTCTGATGTGAAATGGCTGAATTTTGAATCTTACCA 600
 QY 201 AspaspserThrlyserThrlyalalvalalysmetThrProvalilegluValTyr 220
 Db 601 GATATTTCTACTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 660
 QY 221 AspLeuaspIleValaspSerleuGlProvalPheThrleugly-SerlylsleuSerly 240
 Db 661 GACCTTATATAGTGAAGCTCTTTAGAGCCAGCTCTTCACTCGGAAAGT----- 709
 QY 240 slvslvslvslvslvslvslvslvslvslvslvslvslvslvslvslvslvslvslv 260
 |||||

Db 710 -----TCTCAGCAAGAGGCATACCGATGCTGCT 741
 QY 260 uAepLeuSerTrpAsnLysleuilearGAsnValleualaseralaseralaspaanTh 280
 Db 742 TGACCTTCAATGGAATTAAGTAAATGTTTATAGCAAGTCAAGCTGACAAAC 801
 QY 280 rValilleuTrpAspMetSerleuGlylspProalaaaserleuAlvalHisThrAs 300
 Db 802 TGTAAATTCGTGGATATGCTCTTGGGAAACCAAGCAGCTAGCTGCTGACACAG 861
 QY 300 pLysValGlnThrleuGlnPheHisProhegluaIaglnThrleuileSerGlySerly 320
 Db 862 CAAGTCCCAACCTCAGATTCATTCATTTGAAGCAAGACTTATTTCTGGCTCA 921
 QY 320 rAepLysSerValalaleuTyrraspCysargSerProaspGluSerHisargMetTrpAr 340
 Db 922 TGATTAAGTCAAGTGGCTTTGTATGACTGCCAGATCCAGATGAAGCAATGAGGG 981
 QY 340 gPheSerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAl 360
 Db 982 ATTCAGTGGCAGATAGAGAGAGTGAATCACTTTTCACCTTTCATTTCTTGCC 1041
 QY 360 aSerThrAspAspGlyPheValTyrrAsnleuaspalaaargSerAspLyProIlePheTh 380
 Db 1042 CAGTACAGATGAGCGCTTGTATTAATTTGATGACGTCATGATTAACCAATTTTAC 1101
 QY 380 rLeuAsnAlaHisAsnAspGlnIleSerGlyLeuaspLeuSerSerGlnIlelysglyCy 400
 Db 1102 ACTTAATGCACACAAATGAATCTCTGCTTGAATCTTACAGCAATCAAGGCTG 1161
 QY 400 sLeuValThrAlaSerAlaAspLysTyrrVallyslleTrpAspIleleuGlyAspArgPr 420
 Db 1162 TCTGTGACTGCTTACGTGACCAATACGTAAGACTCTGGACATCTTGGAGATGGCC 1221
 QY 420 oSerleuValHisSerArgAspMetlysmetGlyValleuPheCysSerSerCysGlyPr 440
 Db 1222 AAGTCTAAGTCAATTCAGAGCAATGAAGATGGAGTCTCTGTGCTTCATGTTGCC 1281
 QY 440 oAepLeuProPheIleTyrrAlaPheGlyGlyGlnlyslgluGlyLeuArgValTrpAspI 460
 Db 1282 TGATTTGCCATTTATTTATTCCTTTGAGAGTCAAAAGAAAGGCTTCGGGTCTGGATAT 1341
 QY 460 eSerThrValSerSerValasnaGlualaPheGlyArgArgGluArgLeuValleuGlyse 480
 Db 1342 AACCAAGCTCTCTTCAAGTAATGAACATTTGGAACAGAGAGGCTTCTTGGAG 1401
 QY 480 rAlaArgAsnSerSerIleSerGlyProPheGlySerArgSerAspThrProMetG 500
 Db 1402 TGCAGAAATTCATCTAATTAATGAGCCCTTTTGGCAGCAGAGCTCAGATACACCCATGGA 1461
 QY 500 user 501
 Db 1462 GTCT 1465
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RESULT 2

US-10-264-049-376
 ; Sequence 376, Application US/10264049
 ; Publication No. US20040005579A1
 GENERAL INFORMATION:
 ; APPLICANT: Birste et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA133P1
 ; CURRENT APPLICATION NUMBER: US/10/264,049
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/18569
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: US 60/209,467
 ; PRIOR FILING DATE: 2000-06-07
 ; NUMBER OF SEQ ID NOS: 4360
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 376
 ; LENGTH: 2584
 ; TYPE: DNA

ORGANISM: Homo sapiens
US-10-264-049-376

Alignment Scores:

Pred. No.:	5, 93e-241	Length:	2584
Score:	2084.00	Matches:	395
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.94%	Indels:	0
DB:	12	Gaps:	0

US-09-315-355c-10 (1-501) x US-10-264-049-376 (1-2584)

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Qy 107 AspAlaGluThrLeuGluSerLeuGluLeuThrValTyrGlySerAspGln 126
Db 131 GAGGCTAGACTCTGGTGAATCTCTGGCTTACGGCTACGGAATATGATCA 130
Qy 127 AspProTyrValThrLeuLysAspThrGluGlnTyrGluArgGluAspPheLeu 146
Db 191 GATCCTTACGTTACTCTGAAAGATACAAATATACGATGAGATTTCTTGATTA 250
Qy 147 ProSerAspMetLeuValCysGlyArgAlaGluGlnAspGlnCysAsnLeuVal 166
Db 251 CCAGTATATATCTTATAGTTGTGGCCGAGCTGAACAGACATTTAGAGGTG 310
Qy 167 HisValTyrAsnGlnGluAspSerPheTyrValHisAspIleLeuLeuSerAla 186
Db 311 CAGCTTATATACAGAAAGAACTCTTTTATGTAACCATATATACCTCTGCA 370
Qy 187 TyrProLeuSerValGluTyrPleuAsnPheAspProSerProAspAspSerThrGlyAsn 206
Db 371 TATCCTTGAGTGGAGATGCTGAATTTGATCTTACCCAGATGATTTCTACGAAAT 430
Qy 207 TyrIleAlaValGlyAsnMetThrProValIleGluValTyrPheLeuAspIleValAsp 226
Db 431 TACATGCTGTAGAAACATGACCCCTGTTATTAAGTGGGACCTGTGATATAGTGAC 490
Qy 227 SerLeuGluProValPheThrLeuGlySerLysLeuSerLysLysLysLysGly 246
Db 491 TCTTTAAGCCAGCTTCACTGCACTGGAAAGTAACTTTCAAAAAGAAAGAAAGAA 550
Qy 247 LysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTyrAsnLys 266
Db 551 AAGAAAGGTTCTCTCAGCAGAAAGGCAATACGATCTGCTTGAACCTTCAATGAAATAG 610
Qy 267 LeuIleArgAsnValIleAlaSerAlaSerAlaAspAsnThrValIleLeuTyrAspMet 286
Db 611 CTATTCAGAAATGTTTATAGCAAGTGCATCAGCTCAACAACCTGTAATTCGTGGATATG 670
Qy 287 SerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeuGln 306
Db 671 TCCCTGGGAAACAGAGCTAGCTGCTGCTTACACAGACAAAGGCTCCAAACCTCAG 730
Qy 307 PheHisProPheGluAlaGlnThrLeuIleSerGlySerTyrAspLysSerValAlaLeu 326
Db 731 TTTATCATCTTGAAGCAGACACTGATTTCTGGCTCAATATGATAGTACGTGGCTTGG 790
Qy 327 TyrAspCysArgSerProAspGluSerHisArgMetTyrPheSerGlyGlnIleGlu 346
Db 791 TATACCTGCCCAAGTCCAGATGAAGGCAATGATGAGCATTCAGTGGGCAATAGAG 850
Qy 347 ArgValThrTyrAsnHisPheSerProCysHisPheLeuAlaSerThrAspAspGlyPhe 366
Db 851 AGAGTACCTGGAAATCACTTTTCACTTGTATTTCTTGGCCATACAGATGAGGCTTT 910
Qy 367 ValTyrAsnLeuAspAlaArgSerAspLysProIlePheThrLeuAsnAlaHisAsnAsp 386
Db 911 GTATATATATTTGATGACGCTTCAATAGCAATTTTATACCTTATATGCAACAATGAT 970
Qy 387 GluIleSerGlyLeuAspLeuSerSerGlnIleLysGlyCysLeuValThrAlaSerAla 406
Db 971 GAAATCTCTGCTTGTAGCTTACAGCTCAATCAAGGCGTCTCTGTCGATGCTTCAAGCT 1030

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Qy 407 AspLysTyrValLysIleThrAspIleLeuGlyAspArgProSerLeuValHisSerArg 426
Db 1031 GACAAATACGTGAAGATCTGGAGACATCTTAGAGATAGGCCAAGCTTACTTCACTTAG 1090
Qy 427 AspMetLysMetGlyValLeuPheCysSerSerCysCysProAspLeuProPheIleTyr 446
Db 1091 GACATATAAATGGAGATCTCTTCTGTTCTTCAATGTTGCCCTGATTTGCCATTTATTA 1150
Qy 447 AlaPheGlyGlyGlnLysGluGlyLeuArgValTyrAspIleSerThrValSerSerVal 466
Db 1151 GCCTTGGAGGTCAAAAAGAGGCTTCGGCTCGGATATATAGCACAGCTCTTCACTAGTA 1210
Qy 467 AsnGluAlaPheGlyArgArgGluArgLeuValLeuGlySerAlaArgAsnSerSerIle 486
Db 1211 AATGAAGCAATTTGGAAGACGAGAGAGCTTGTCTTGGAGATGCAAGAAATTCATATAT 1270
Qy 487 SerGlyProPheGlySerArgSerSerAspThrProMetGluSer 501
Db 1271 AGTGGCCCTTTTGGCAGCAGAGCTCAGATACACCATGAGTCT 1315

RESULT 3
US-10-062-674-1561
; Sequence 1561, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1561
; LENGTH: 3024
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 124921.6
; FEATURe:
; NAME/KEY: unsure
; LOCATION: (1) ... (3024)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-1561

Alignment Scores:
Pred. No.: 1,31e-201 Length: 3024
Score: 1759.50 Matches: 429
Percent Similarity: 81.64% Conservative: 20
Best Local Similarity: 78.00% Mismatches: 49
Query Match: 66.65% Indels: 53
DB: 12 Gaps: 9

US-09-315-355c-10 (1-501) x US-10-062-674-1561 (1-3024)

Qy 4 SerArgGlnValThrCysVal---AlaTyr-ValArgCysGlyValAlaLysGluThrPr 22
Db 131 GCCCGCCAAATGATCGTTGGTAGGCTGTGAGTCCCTGGGGGTGCCAAAGACACC 190
Qy 22 aaPlyValGluLeuSerLysGluGluValLysArgLeuIle-AlaGluAlaLysGluLul 42
Db 191 AGCAAGGTAGAGCTAGTAAAGAAAGTAAACCCCTCATCTGCTGAGGCAAGAGAGA 250
Qy 42 yslLeuGlnGluGluGlyGlySerAspGluGlnGluThrGlySerProSerGluAspG 62
Db 251 AATTGAGAAAGAGGTGGTGGAGTGAAGAGACAGGCACTTCCAGAAAGATG 310
Qy 62 lymetGln-----SerAlaArgThrGlnAlaArgProArgGluProL 76
Db 311 GCATGAGATGTGCCAGCGCCAGCCCACTGCGCCCAATGATGATAGCCCTTG 370

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Qy 76 euGluAsp-GlyAspPro-GluAspAspArgThrLeuAsp-AspAspGluLeuAlaGluT 95
Db 371 TGAAGCATGTGTGACCCATGAGATGACAGACCGCTTGTAATATGAGCTGCTGAGT 430
Qy 95 YrAspLeuAspLysThrAspGluGluGlyAspProAspAlaGluThrLeuGly----- 112
Db 431 ACGACTTAGAATATGATGAGAGAGGTGACCCAGATGCTGAACACTCTGGCTGAGATC 490
Qy 113 -----GluSerLeuLeuGlyLeuThrValTyrGlySerAsnAspGlnAspProTyr--V 130
Db 491 TCTCTTAGGCTCTTAACGGGCTTAACAGGGGAGATATAGTCAAGAGACTCTTAGCT 550
Qy 130 alThrLeuLysAspThrGluGlnTyrGluArgGluAspPheLeuIleLysProSerAsp 150
Db 551 TACTTCTGAAGATACAGAACATATGAACTGAAGATTTCTTATTAAGCCCGTGATT 610
Qy 150 sn-LeuIleValCysGlyArgAlaGluGlnAspGlnCysAsnLeuGluValIleValTyr 169
Db 611 ATTCTTATAGTTTGCGCCGAGCTGAACAGACAGAGTCAATTTAAGAGTGCATGTTAT 670
Qy 170 AsnGlnGluGlu-AspSerPheTyrValIleHisAspIleLeuLeuSerAlaTyrProLe 189
Db 671 AATCCAGAGAAAGAACTTTTATGTCACCAAGATATCTCTTGCTGCTGCTCT 730
Qy 189 uSerValGluTrpLeuAsnPheAspProSerProAspAspSerThr-GlyAsnTyrIleA 209
Db 731 GAGGTGGAATGGCTGAATTTGATCTCAAGCCAGATGATTTCTAGGAAATTAATGATG 790
Qy 209 laVal-GlyAsnMetThrProValIleGluValIleTrpAspLeuAspIle-Val----- 225
Db 791 CTGTAGGGAACAAGACCCCTGTATGAAAGTGTGGACCTGTGAATATTATTAAGGGGTT 850
Qy 226 -----AspSerLeuGluProValPheThrLeu-GlySerLysLeuSerLysLysL 242
Db 851 TTGGGGGGGGGACCTTTAGACCAAGTCTTACACTGCGGAGAGTAACTTTCAAAAAAGA 910
Qy 242 YrLysLysLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaVal-LeuAsp 261
Db 911 AGAAAAAGAAAGAAAGAGTTCCTCAGCAAGAGGCATACCGATGCTGCTCGTTGAC 970
Qy 262 LeuSerTrp-AsnLysLeuIleArgAsnValLeu---AlaSerAlaSerAla-AspAsn 280
Db 971 CTTCATGAGGAATAGCTAATACGACAAATGTTTAAAGCAAGTCACTGACGACACACA 1030
Qy 280 hrValIleLeuTrpAspMetSer-LeuGlyLysPro-AlaAlaSerLeuAlaValIleSt 299
Db 1031 CTGTAAATTCGTGGATATGTCCTTGCGGAAACACAGACACTGACCTCGCTGACAC 1090
Qy 299 rAspLysValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSer-Glys 319
Db 1091 AGACAAAGTCCAAACACTGACGATTCACTTGAAGCACAGACTGATTTCTGGGCT 1150
Qy 319 erTyrAspLysSerValAlaLeu---TyrAspCysArgSerProAsp---GluSerHis 336
Db 1151 CATATGATTAAGTCTAGTGGCTTTGTATTGACTCCGCAAGTCCAGATTGAAAGCCATC 1210
Qy 337 ArgSerTrpArgPheSerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCys 356
Db 1211 CGAATGTGGCATTACAGTGGGCAATGAGAGAGTGTCTGGAATCACTTTCACTTGT 1270
Qy 357 HisPheLeuAlaSerThrAspAsp-GlyPheValTyrAsnLeuAspAlaArgSerAspLys 376
Db 1271 CATTTCTTGGCAGTACAGATGACGGCTTTGTATATATATTTGATGACACTTACAGTAA 1330
Qy 376 spIlePheThrLeuAsnAlaHisAsnAspGlnIleSerGlyLeuAspLeuSerSerGly 396
Db 1331 GCCAATTTTTCACCTTAATGACACAAATGATGAATCTCTGCTTATCTTACACTCA 1390
Qy 396 nIle-LysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleTrpAspIleL 416
Db 1391 AATCCAAGGCTGTCTGTGACTCTTCACTGCAAAATAGTGAAGATCTGGGAAACATCT 1450
Qy 416 euGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPhe-Cys 435

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Db 1451 TAGAGATAGCCCAAGCTCTGATTCATTCAGGACATGAAAGGAGTCTGCTGCTG 1510
Qy 436 SerSerCysCysProAspLeuPro---PheIleTyrAlaPheGlyGlyGlnLysGly 454
Db 1511 GTGTCATGTGCTCCCTGAGTTCCTCAATTTATGTATGTGTGCA-GGTCAAAAGAAAGG 1569
Qy 455 LeuArgValTrp-AspIleSerThrValSerSerValAsn---GluAlaPheGlyArg 473
Db 1570 CTTCGGGCTGGGAGATATTAAGACACAGCTCTTCCAGAAATGAGACATTTTGAAGACG 1629
Qy 473 gGlu-ArgLeuValIleGlySer-AlaArgAsnSerSer--IleSerGlyProPheGlyS 492
Db 1630 AGAGAGGCTGTGTTCTTGGGACCTGCAAGAAATTCATTTATTCAGTGGCCCTTTGGCA 1689
Qy 492 erArgSerAspThr-ProMetGluSer 501
Db 1690 GCAGAGCTCAGATACCCCAATGAGATCC 1719

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RESULT 4

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US-10-128-714-2208
: Sequence 2208, Application US/10128714
: Publication No. US20030119013A1
: GENERAL INFORMATION:
: APPLICANT: Jiang, Bo
: APPLICANT: Hu, Wengji
: APPLICANT: Tishkoff, Daniel
: APPLICANT: Zamudio, Carlos
: APPLICANT: Broshkin, Alexey M
: APPLICANT: Lemieux, Sebastien M
: TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
: FILE REFERENCE: 10182-018-999
: CURRENT APPLICATION NUMBER: US/10/128, 714
: CURRENT FILING DATE: 2002-04-23
: PRIOR APPLICATION NUMBER: US 60/285,697
: PRIOR FILING DATE: 2001-04-23
: PRIOR APPLICATION NUMBER: US 60/287,066
: PRIOR FILING DATE: 2001-04-27
: PRIOR APPLICATION NUMBER: US 60/295,890
: PRIOR FILING DATE: 2001-06-05
: PRIOR APPLICATION NUMBER: US 60/303,899
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: US 60/316,362
: NUMBER OF SEQ ID NOS: 8603
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2208
: LENGTH: 1620
: TYPE: DNA
: ORGANISM: Aspergillus fumigatus
US-10-128-714-2208

```

Alignment Scores:

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Pred. No.: 2,08e-102 Length: 1620
Score: 935.50 Matches: 207
Percent Similarity: 56.73% Conservative: 88
Best Local Similarity: 39.81% Mismatches: 196
Query Match: 35.44% Indels: 29
DB: Gaps: 10

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US-09-315-355c-10 (1-501) x US-10-128-714-2208 (1-1620)

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Qy 4 SerArgGlnValThrCysValAlaTrpValArgCysGlyValAlaLysGluThrProAsp 23
Db 4 TCTTATGATGCTCTACGACCGCTTGCGGCGGAGAGTCCCTCCCAATTCCTTACC 63
Qy 24 LysValGluLeuSerLysGluGluValLysArgLeuIleAlaGluAlaLysGluLysLeu 43
Db 64 AAATATGAGATTACAGAGAGGAAATGAAACCGGATATCCAAAGTCCGCTCGAATGCACTC 123
Qy 44 GlnGluGluGlyGlySerAspGluGluGluThrGlySerProSerGluAspGlyMet 63

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Db      124 GAAGAGCCCGGCTGATCTGAGGCTGCCAGGAGGAAAG---GACCAAGACGGCGAG 180
Qy      64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
Db      181 ACCATGAGAGAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy      84 AspArgThrLeu-----AspAspAspGluLeuAlaGluTyrAspLeuAspLys 99
Db      241 AAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy      100 TyrAsp---GluGluGluAspProAspAlaGlu-----ThrLeuGluGluSerLeuLeu 116
Db      301 TAGCAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy      117 GlyLeuThrValTyrGlySerAspAspGlnAspProTyrValThrLeu---LysAspThr 135
Db      361 TCGCTAGCAGTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 420
Qy      136 GluGlnTyrGluArgGluAspPheLeuIleLysProSerAspAspLeuIleValCysGly 155
Db      421 GAGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy      156 ArgAlaGluGluAspGlnCysAsnLeuGluValHisValTyrAsnGlnGluAspSer 175
Db      481 AAGGTGAGGATGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGT 540
Qy      176 PheTyrValHisAspIleLeuLeuSerAlaTyrProLeuSerValGluTyrLeuAsn 195
Db      541 CTTTACGTGACACGACGATTTATCTGCGCCCATCTTCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy      196 PheAsp-----ProSerProAspAspSerThrGlyAsnTyrIleAlaValGlyAsn 212
Db      601 TTCCCTGTGGCGCACACGAGATGACCGGACTACCGGCAATTCGTGGCCGTGAGAAC 660
Qy      213 MetThrProValIleGluValTyrAspLeuAspIleValAspSerLeuGluProValPhe 232
Db      661 ATGAGGCCGACATTTGAGTCTGGACCTGGACATTTGCTGACCTGACCTGACCTGACCTG 720
Qy      233 ThrLeuGly-----SerLysLeuSerLysLysLysLysLysLysLysLysLysLys 245
Db      721 ATCTGAGGTGACGGCGGTGCGGAGCTGAGGAGACATGAAGAGGCTTAAAGATCCAG 780
Qy      246 GlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTyrAsn 265
Db      781 AAGAGAGACCAAGGAGATGAGAGATTCACGTCGACCGGTGCTGGCTGGCTGGCAAC 840
Qy      266 LysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuTyrAsp 285
Db      841 CGCCAAACACCGCATCTGCTTGCATCTGCATCCGCTGATCGTAAACCTCTGGGAC 900
Qy      286 MetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeu 305
Db      901 CTCAACACCGCCAAAGTGGCCAAATCTTACACCCATATACGAGCAAGGTGTGCTGCTG 960
Qy      306 GlnPheHisProPheGlnAlaGlnThrLeuIleSerGlySerTyrAspLysSerValAla 325
Db      961 GACTGGACCGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy      326 LeuTyrAspCysArgSerProAspGluSerHisArgMetTyrArgPheSerGlyGlnIle 345
Db      1021 GCGGCAAGATGAGAGAGTCCCGAGCGCAAGACGGG---TGGGAGATGAGATGCCAGAGTC 1077
Qy      346 GluArgValThrTyrAsnHisPheSerProCysHisPheLeuAlaSerThrAspAspGly 365
Db      1078 GAGAGATGCGGCTGAGATTTACAGACCCAACTTTCTTATGTCCACACAGATGCCGCT 1137
Qy      366 PheValTyrAsnLeuAspAlaArgSer-----AspLysProIle 378
Db      1138 ATGCTTACCGCTACGATGCTTGAACATCCCTGCAACGCAAGAGATGAAACCGCTC 1197
Qy      379 PheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSerGlnIleLys 398
Db      1198 TGGACCTGACGAGCGCATGACACCTCTGTGTCATCTTTGACATCAACCTGCAATTCCT 1257

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Qy      399 GlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleTyrAspIleLeuGlyAsp 418
Db      1258 GGCTTCCTGTAACCGGATCAACGATTAAGCAAGTCAACTATGAACTCGAAGATGCG 1317
Qy      419 ArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCysSerCys 438
Db      1318 CGGCTTACGATGATGCTCTCGGCTGAGTACGAGTGTGTAAGTGTGTTTCGACCACTTC 1377
Qy      439 CysProAsp-----LeuProPheIleTyrAlaPheGlyGlyGlnLysGluLeuArg 456
Db      1378 GCTTCTGACACAGAGTGGCTTCGCGTGGCGGTGCTGCGACGACGAGAACCGCTCCAG 1437
Qy      457 ValTyrAspIleSerThrValSerSerValAsnGluAlaPheGlyArgArgGluArgLeu 476
Db      1438 ATCTGGACACCTCGACCAACGAGCGCTTCGTAAGCTTTTGTGCTCGCATGCCGCGC 1497
Qy      477 ValLeuGlySerAlaArgAsnSerIleSerGlyProPheGlySerArgSerAsp 496
Db      1498 CTGGAAGCGGAGGTCAAGAGCGCACATCGAGTGCAGACCGACGATGATGATGAT 1557

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RESULT 5

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US-10-128-714-7208
; Sequence 7208, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wench
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskinin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7208
; LENGTH: 1629
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
; US-10-128-714-7208

```

Alignment Scores:

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Pred. No.: 1,11e-101 Length: 1629
Score: 929.50 Matches: 206
Percent Similarity: 56.54% Conservative: 88
Best Local Similarity: 39.62% Mismatches: 197
Query Match: 35.21% Indels: 29
DB: 15 Gaps: 10

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US-09-315-355c-10 (1-501) x US-10-128-714-7208 (1-1629)

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Qy      4 SerArgGlnValThrCysValAlaTyrPValArgCysGlyValAlaLysGluThrProAsp 23
Db      4 TCTTATGATCTACTACGACCGCTTGCGTGGCGGAGAGTCCGCTCCCAATTCCTTACC 63
Qy      24 LysValGluLeuSerLysGluGluValLysArgLeuIleAlaGluAlaLysGluLysLeu 43
Db      64 AATATATGAGATTGACGAGAGGAAATGAACCGGATATCCAAAGCTCGCTGATGACAGCTC 123

```

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QY 44 GlnGluGluGlyGlySerAspGluGluThrGlySerProSerGluAspGlyMet 63
Db 124 GAAGAGCCCGAGGCTGATCTGAGGCTGCCAGGAAGAAAG---GACCGAGAGCGGCGAG 180
QY 64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
Db 181 ACCATGAGGAGGATCAGAAAGAGAAAGCCCAAGACCGGATGAGGAGGATCCGAGAGAA 240
QY 84 AspArgThrLeu-----AspAspAspGluLeuAlaGluTyrAspLeuAspLys 99
Db 241 AAGAGAGGAAGAGAACAGTTTCAATAGATGATGAGATTTGAAGAAATGACCTTGATCAC 300
QY 100 TyrAsp---GluGluGlyAspProAspAlaGlu-----ThrLeuGlyLysLeuLeu 116
Db 301 TACGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 117 GlyLeuThrValTyrGlySerAspGluAspProTyrValThrLeu---LysAspThr 135
Db 361 TCGGTAGCGTACCAACCAACGAGGAGATCCATACCTTGATGATGATGATGATGATGATGAT 420
QY 136 GluGlnTyrGluArgGluAspPheLeuLeuLysProSerAspAspAlaLeuValCysGly 155
Db 421 GAGGATGAGAGAGAGAGAGATTCGATGATCTTCCACCGCAACCTTCTTCTTCTTCTTCT 480
QY 156 ArgAlaGluGlnAspGlnCysAsnLeuGluValHisValTyrAsnGlnGluGluAspSer 175
Db 481 AAGGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 176 PheTyrValHisAspPheLeuLeuSerAlaTyrProLeuSerValGluThrLeuAsn 195
Db 541 CTTTACGTCACCAACGATTTATCTGCGCCCATCTCTGCTGCTGCTGCTGCTGCTGCTGAT 600
QY 196 PheAsp-----ProSerProAspAspSerThrGlyAsnTyrLeuAlaValGlyAsn 212
Db 601 TTCCCTGTGGCGCACACAGGAGATGACCGGACCTACCGGCAATTCGTGGCGGTAGGAAAC 660
QY 213 MetThrProValIleGluValTyrAspLeuAspIleValAspSerLeuGluProValPhe 232
Db 661 ATGAGGCGCGCATTTGAGGTCTGGGACCTGGAATTTGCGATCGATGATGATGATGATGAT 720
QY 233 ThrLeuGly-----SerLysLeuSerLysLysLysLysLysLysLysLysLys 245
Db 721 ATCTGTGATCGAGGCGGCTGCGAGCTCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 246 GlyLysLysSerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTyrAsp 265
Db 781 AAGAGAGCAAGGAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 266 LysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuTyrAsp 285
Db 841 CGCCAGACCGCATTCGCTTGCATTCGATCCGCTGATCGTAAACCTCTGGGAC 900
QY 286 MetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeu 305
Db 901 CTCAACACCGGCAAGTGGCGCAATCTTACACCCATCATGAGCAAGTGTGCTCGTG 960
QY 306 GlnPheHisProPheGluAlaGlnThrLeuLysSerGlySerTyrAspLysSerValAla 325
Db 961 GACTGGACCGCTTAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 326 LeuTyrAspCysArgSerProAspGluSerHisArgMetTyrAspPheSerGlyGlnIle 345
Db 1021 GCGGAGAGCATGAGAGCTCCGAGCGGAAAGCGGG---TGGGAGTGGATGCGGAGCTC 1077
QY 346 GluArgValThrTyrAsnHisPheSerProCysHisPheLeuAlaSerThrAspAspGly 365
Db 1078 GAGATGTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1137
QY 366 PheValTyrAsnLeuAspAlaArgSer-----AspLysProIle 378
Db 1138 ATGCTTACCGCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
QY 379 PheThrLeuAsnAlaHisAsnAspGluLysSerGlyLeuAspLeuSerSerGlnIleLys 398

```

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Db 1198 TGAGACCTTGAGGCGGATGACACCTCTGTCTATCTTGAACATCAACCTTGCCATTCT 1257
QY 399 GlyLeuValThrAlaSerAlaAspLysTyrValLysIleThrAspIleLeuGlyAsp 418
Db 1258 GGCCTCTCTGTAACCGGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 1317
QY 419 ArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCysSerSerCys 438
Db 1318 CGGCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
QY 439 CysProAsp-----LeuProPheIleTyrAlaPheGlyGlyGlnLysGluGlyLeuArg 456
Db 1378 GCTCTGACCAACGAGTGTGCTTCGCTGCGGTGAGCTGCGACGAAAGGAAACCGTCCAG 1437
QY 457 ValTyrAspIleSerThrValSerValAsnGluAlaPheGlyArgArgGluArgLeu 476
Db 1438 ATCTGGACACCTCGACCAACGAGCGCTTCGTAAGACTTTTGTCTGCAATGCCCGCC 1497
QY 477 ValLeuGlySerAlaArgAsnSerSerIleSerGlyProPheGlySerArgSerAsp 496
Db 1498 CTGGAAGCGGAGGTCAAGAGAGCCACATCGAGTCAAGCCGAGCATGATGATCGAT 1557

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RESULT 6

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US-10-128-714-6208
Sequence 6208, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:

```

```

APPLICANT: Jiang, Bo
APPLICANT: Hu, Meng
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroskin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OR INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128, 714
CURRENT FILING DATE: 2002-04-23
PRIORITY APPLICATION NUMBER: US 60/285,697
PRIORITY FILING DATE: 2001-04-23
PRIORITY APPLICATION NUMBER: US 60/287,066
PRIORITY FILING DATE: 2001-04-27
PRIORITY APPLICATION NUMBER: US 60/295,890
PRIORITY FILING DATE: 2001-06-05
PRIORITY APPLICATION NUMBER: US 60/303,899
PRIORITY FILING DATE: 2001-07-09
PRIORITY APPLICATION NUMBER: US 60/316,362
PRIORITY FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6208

```

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LENGTH: 1697
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-128-714-6208

```

Alignment Scores:

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Pred. No.: 4.11e-99 Length: 1697
Score: 908.50 Matches: 207
Percent Similarity: 54.33% Conservative: 88
Best Local Similarity: 38.12% Mismatches: 196
Query Match: 34.41% Indels: 53
DB: 15 Gaps: 10

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US-09-315-355c-10 (1-501) x US-10-128-714-6208 (1-1697)

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QY 4 SerArgGlnValThrCysValAlaTyrValArgCysGlyValAlaLysGluThrProAsp 23
Db 4 TCTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 63
QY 24 LysValGluLeuSerLysGluGluValLysArgLeuIleAlaGluAlaLysGluLysLeu 43

```

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Db      64 AATATGAGATTGACGAGGAGAAATGACCGGATATTCAGCTTCGCTCGGATCGACGTC 123
Qy      44 GlnGluGluGlyGlyGlySerAspGluGluGluThrGlySerProSerGluAspGlyMet 63
Db      124 GAAAGAGCCCGAGGTGATCTGAGAGCTGCCGAGGAGGAAAG---GACACGAGAGCGGGAG 180
Qy      64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
Db      181 ACCATGAGGAGGATCAGAGAGGAGAAAGCCAGACCGGATGAGGAGCATTCGAGGAA 240
Qy      84 AsparGlnr----- 86
Db      241 AAGAGG-AAAACAAGTTCAATGAGTAGCTCAAGCTTAACTGTCGCGATCTTCATA 299
Qy      87 -----LeuAspAspGluLeuAlaGluTyrAsp 96
Db      300 TAGACAAAGGCTAACACCTGCTCGCTTGTCTTGTATGTAAGATTGAAGAAATACGAC 359
Qy      97 LeuAspLysTyrAsp---GluGluGlyAspProAspAlaGlu-----ThrLeuGlyGlu 113
Db      360 CTGATCATCTACGACAGATGATGAGGTGATGAGATGAGAGAGATCATCATGTCGGA 419
Qy      114 SerLeuLeuGlyLeuThrValTyrGlySerAspGlnAspProTyrValThrLeu--- 132
Db      420 AACGTCAAAGTCGTACGCTACCAACCAACGAGAGATCATCTTGTATACCG 479
Qy      133 LysAspThrGluGlnTyrGluArgGluAspPheLeuIleLysProSerAspAsnLeuIle 152
Db      480 GAAAGAGAGAGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
Qy      153 ValCysGlyArgAlaGluGlnAspGlnCysAsnLeuGlnValHisValTyrAsnGlnGlu 172
Db      540 CTTCAGAGTAGTGTCGAGATGAGGTGCGCATCTTGAAGCTTACGTTACGAGAGACAG 599
Qy      173 GluAspSerPheTyrValHisHisAspIleLeuLeuSerAlaTyrProLeuSerValGlu 192
Db      600 GAGCGCAAGCTTTCAGTGCACACGACATTAAGTGCAGCCGCTCTGCTGCTGAA 659
Qy      193 TrpLeuAsnPheAsp-----ProSerProAspAspSerThrGlyAsnTyrIleAla 209
Db      660 TGGCTGGATTTCCCTGTTGGCGCACACAGGATGACCGGATACCGGGAATTTGCTGCC 719
Qy      210 ValGlyAsnMetThrProValIleGluValTyrAspLeuAspIleValAspSerLeuGlu 229
Db      720 GTAGGAACCATGAGCCCGACATTAAGGTCTGGAGCTCGACATTTGTCATCGCATGAC 779
Qy      230 ProValPheThrLeuGly-----SerLysLeuSerLysLys 242
Db      780 CCAAAAGCCATCTGGGTCAAGGCGGTGCGAGCTCGAGGAGACATGAAAGGCTTAA 839
Qy      243 LysLysLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeu 262
Db      840 AAGTCCAAGAAAGAAAGCAAGGCGGATGACGATTCACGTCGACTCGCTGCTGCCCTG 899
Qy      263 SerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAspThrValIle 282
Db      900 GCTGAAACCCGCAACACCGCATCTGCTGTCATTCGATCCGTCGATCGATACCTTAAA 959
Qy      283 LeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysVal 302
Db      960 CTCTGGAGACTCAACACCGCCCAAGTGCCTTACACCCATCATACGACACCAAGGTG 1019
Qy      303 GlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerTyrAspLys 322
Db      1020 TGCTGCTGAGCTGGACCTTAAGAGACTACCGTTCTCTCACCGAGTTACGATGCT 1079
Qy      323 SerValAlaLeuTyrAspCysArgSerProAspGluSerHisArgMetTrpArgPheSer 342
Db      1080 ACCGTGTGGCGGCGAGATGAGAGCTCCGACCGGAAAGCCGG---TGGGAGATGAT 1136
Qy      343 GlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSerThr 362
Db      1137 GCCGACGTGAGAAATGTGGGTGGATATTTCAGACCCAACTTCTTATGTACACACA 1196

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Qy      363 AspAspGlyPheValTyrAsnLeuAspAlaArgSer-----Asp 375
Db      1197 GATGCCGATATGCTATACCCCTACGATGTTGAAACATCCCTGCAACGCCAAAGAAATCG 1256
Qy      376 LysProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSer 395
Db      1257 AAACCGGTGAGACCTCGACGCGCATGACACTCTGTGTATCTTTGACATCAACCTT 1316
Qy      396 GlnIleLysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleTrpAspIle 415
Db      1317 GCCATTCCTGCTCTTCTCTCGTACCGGATCAACGATTAAGCAATCAAGTATGAACGTC 1376
Qy      416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCys 435
Db      1377 GAGATGCCCGGCGCTAGCATGTCGTCCTCGTAAGATGACCTGTGTAAGTGTTCG 1436
Qy      436 SerSerCysCysProAsp-----LeuProPheIleTyrAlaPheGlyGlyGlnGlu 453
Db      1437 ACCACCTTCGCTCTGCAACGAGGTGCTTCGCTGCGGTAGCTGGACCAAGGGA 1496
Qy      454 GlyLeuArgValTyrAspIleSerThrValSerSerValAsnGluAlaPheGlyArgArg 473
Db      1497 ACCGTCGATCTGGGACACCTGACCAACGAGCCGTTGTAGAGCTTTGTGTCTCGC 1556
Qy      474 GluArgLeuValLeuGlySerAlaArgAsnSerSerIleSerGlyProPheGlySerArg 493
Db      1557 ATGCCCGCCCTGGAAGCGGAGGTCAAGAGAGCGACATCGAGTGCAGACGATGAT 1616
Qy      494 SerSerAsp 496
Db      1617 GAATCGGAT 1625

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RESULT 7

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US-10-128-714-208
; Sequence 208, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Mengli
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OR INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OR INVENTION: Methode of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 208
; LENGTH: 3617
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-208

Alignment Scores:
Pred. No.: 1,36e-98 Length: 3617
Score: 908.50 Matches: 207
Percent Similarity: 54.33 Conservative: 88
Best Local Similarity: 38.12 Mismatches: 196
Query Match: 34.41% Indels: 53

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DB: 15 Gaps: 10

US-09-315-355C-10 (1-501) x US-10-128-714-208 (1-3617)

QY 4 SerArgGlnValThrCysValAlaThrValArgCysGlyValAlaIleValGluThrProAsp 23

DB 1004 TCTTCTATGATCAGTACGACCGCTGGGTGGCGGGAGTGGCTGCGCCCAATTCCTTACC 1063

QY 24 LysValGluLeuSerGlyGluValLysArgLeuIleAlaGluAlaValGluIleLeu 43

DB 1064 AAATATGATGATGACGAGGAGGAAATGAACCGATATCCAGCTCGCTCGATGACGCTC 1123

QY 44 GlnGluGlnGlyGlyGlySerAspGluGluGlnThrGlySerProSerGluAspGlyMet 63

DB 1124 GAAGCGCCGAGGATGATCTGAGGCTCCAGGAGGAAAG---GACCAGACGCGCGAG 1180

QY 64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83

DB 1181 ACCATGAGAGGATCAAGAGAGAGAGAGCCCAAGACCGGATGAGAGAGATTCGAGAGAA 1240

QY 84 AspArgThr----- 86

DB 1241 AAGAAAGG-AAAGACAGTTCAATGAGTGAAGTCTTAAGCTTACTGTCGATCTTATA 1299

QY 87 -----LeuAspAspAspGluLeuAlaGluThrAsp 96

DB 1300 TAGACAAGGCTAACCTGATCTCGCTTGTAGTGAATTTGAAGAAATACGAC 1359

QY 97 LeuAspLysIleAsp---GlnGluGluAspProAspAlaGlu-----ThrLeuGlyGlu 113

DB 1360 CTATATCACTACGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1419

QY 114 SerLeuGlnGlyLeuThrValIleGlySerAspGlnAspProGlyValThrLeu--- 132

DB 1420 AACGTCAGTGGCTTACGCTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1479

QY 133 LysAspThrGlnGlnIleGluArgGluAspPheLeuIleLysProSerAspAspLeuIle 152

DB 1480 GAAGAGAAGAGAGATGAAG 1539

QY 153 ValCysGlyArgAlaGluGlnAspGlnCysAsnLeuGluValIleValIleValIleVal 172

DB 1540 CTTCCAGGTAAAGTCCAGAGATGAGTGGCCCATCTTGAAGCTTACGCTTACGAGACAG 1599

QY 173 GlnLysSerPheThrValIleHisAspIleLeuLeuSerAlaIleProLeuSerValGlu 192

DB 1600 GAGGCGAACCTTTACGTGACCAACGATATGCTGCCCGCCATCTCTGTGCTTGA 1659

QY 193 TrpLeuAsnPheAsp-----ProSerProAspAspSerThrGlyAsnIleAla 209

DB 1660 TGGCTGAGATTTCCGCTGGCGCACACGATGACCGGATACCGGCAATTCGTGGCC 1719

QY 210 ValGlyAsnMetThrProValIleGluValIleThrAspLeuAspIleValAspSerLeuGlu 229

DB 1720 GTAGAACCAATGAGCCCGACATGAGTCTGGGACCTGGACATTTGCTGATCGATGAC 1779

QY 230 ProValPheThrLeuGly-----SerLysLeuSerLysLysLys 242

DB 1780 CCAAAAGCCATCTGGGTGACGAGGCGGTGGAGCTCCAGGAGACATGAAGAGGCTTAA 1839

QY 243 LysLeuLysGlyLysLysSerSerSerAlaGluGlnHisThrAspAlaValLeuAspLeu 262

DB 1840 AAGTCCAAAG 1899

QY 263 SerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIle 282

DB 1900 GCTCAAAACCCCAACCCCAATCTGCTGATCTGATCGCTGATCGTAAACCGTAA 1959

QY 283 LeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValIleHisThrAspVal 302

DB 1960 CTCTGGAGCTCAACCCGAGAGGCGCCAAATCTTACCCATCAACGAGAGAGAGAGAG 2019

QY 303 GlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerLysAspLys 322

DB 2020 TGGCTGCTGACGACGACACCTTAAGAGATACCGTTCTCTCCACCGGATTTACGATCGT 2079

QY 323 SerValAlaLeuThrCysArgSerProAspGluSerHisArgMetTrpAspPheSer 342

DB 2080 ACCGTGTGGCGGACAGACATGAGAGCTCCGAGCGCAAGCGCG---TGGGAGTGAT 2136

QY 343 GlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSerThr 362

DB 2137 GCGAGCTGACAGAAATGGCGGTGGATATTCAGCACCCAAATCTTCTATGTCACACACA 2196

QY 363 AspAspGlyPheValIleThrLeuLeuAspAlaArgSer-----Asp 375

DB 2197 GATGCGCGTGTGTCTTACCCCTACGATGTTGCAAAATCCCTGCAACGCCAAAGAAATCG 2256

QY 376 LysProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSer 395

DB 2257 AAACCGGTCTGACACCTTGACGCGCATGACACCTCTGTGTCATCTTTGATCAATCAACCT 2316

QY 396 GlnIleLysGlyCysLeuValThrAlaSerAlaAspLysIleValIleTrpAspIle 415

DB 2317 GCCATTCCTGCTTCTCTCGTAAACCGGATCAACGATTAAGCAATCAAGTATGAAAGCTC 2376

QY 416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCys 425

DB 2377 GAGAAATGCGCGGCTTACGATGCTGCTCGCTGATGATGACGCTTGAAGGTGTTTCG 2436

QY 436 SerSerCysSerProAsp-----LeuProPheIleThrAlaPheGlyGlnLysGlu 453

DB 2437 AACACCTTCTGCTCTGACCAAGAGTGGCTTCCGTTGGCGGTAGCTGACGACCAAGGCA 2496

QY 454 GlyLeuArgValTrpAspIleSerThrValSerSerValAsnGluAlaPheGlyArgArg 473

DB 2497 ACCGTCAAGTCTGGGACACCTGACCAACGAGCGGTTGTAGAGTTTGTGTCTCGC 2556

QY 474 GlnArgLeuValLeuGlySerAlaArgAsnSerSerIleSerGlyProPheGlySerArg 493

DB 2557 ATGCCCCGCTCGGAGAGCGGATCAAGAGCGCACATCGAGTGCAGCCGACGATGAT 2616

QY 494 SerSerAsp 496

DB 2617 GAATCGGAT 2625

DB 2617 GAATCGGAT 2625

RESULT 8

US-10-128-714-5208

Sequence 5208, Application US/10128714

Publication No. US20030119013A1

GENERAL INFORMATION:

APPLICANT: Jiang, Bo

APPLICANT: Hu, Weng

APPLICANT: Tishkoff, Daniel

APPLICANT: Zamudio, Carlos

APPLICANT: Eroshekin, Alexey M

APPLICANT: Lemieux, Sebastien M

TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

FILE REFERENCE: 10182-018-999

CURRENT APPLICATION NUMBER: US/10/128, 714

CURRENT FILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: US 60/285,697

PRIOR FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: US 60/287,066

PRIOR FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: US 60/295,890

PRIOR FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: US 60/303,899

PRIOR FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: US 60/316,362

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 8603

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5208

LENGTH: 3697


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; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
; US-10-128-714-5208

Alignment Scores:
Pred. No.: 1.41e-98      Length: 3697
Score: 908.50           Matches: 207
Percent Similarity: 54.33%      Conservative: 88
Best Local Similarity: 38.12%    Mismatches: 196
Query Match: 34.41%           Indels: 53
DB: 15                  Gaps: 10

US-09-315-355c-10 (1-501) x US-10-128-714-5208 (1-3697)

Qy      4 SerArgInValThrCysValAlaTrpValArgCysGlyValAlaIysGluThrProAsp 23
Db      1004 TCTTCTATGATCACTACGACCGCTTGGGTGCGGGGAGTCCGTGCCCAATCCCTACC 1063

Qy      24 LysValGluLeuSerLysGluValLysArgLeuLeaIaGluAlaLysGluLysLeu 43
Db      1064 AAATATAGATTGACGAGGAGAAATGAAACCGGATATCCAAAGCTCGCTCGATGACAGCTC 1123

Qy      44 GlnGluGluGlyGlySerAspGluGluGluThrGlySerProSerGluAspGlyMet 63
Db      1124 GAAGAGGCCCGAGGCTGATCTGAGGCTGCCAGGAAAGAAAG--GACCAAGAGCGGAG 1180

Qy      64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
Db      1181 ACCATGAGAGAGATCGAAGAGAGAAAGCCCAAGACCGCATGAGAGACGATTCGAGAGAA 1240

Qy      84 AspArgThr-----
Db      1241 AAGAAAGG-AAAAGACAGTTTCAATGATGATGCTAAGCTTAGTGTCCGATCTTCATA 1299

Qy      87 -----
Db      1300 TAGACAAAGGTAACACTGCATCTCGCTTGTGTTAGTATGAAAGATTGAAATACGAC 1359

Qy      97 LeuAspLysTrpAsp---GluGluGlyAspProAspAlaGlu-----ThrLeuGlyGlu 113
Db      1360 CTGTGATCACTACGACGATGATGAGTGTAGAGATGAGAGAAAGATACCATCTTGGGA 1419

Qy      114 SerLeuGluGlyLeuThrValTrpGlySerAsnAspGlnAspProTrpValThrLeu--- 132
Db      1420 AACGTCAAGTCGCTACGCTACCAACCAACGAGAGAAATCATCTTGTGATACCG 1479

Qy      133 LysAspThrGluGluTrpGluArgGluAspPheLeuLeuLysProSerAspAsnLeuLe 152
Db      1480 GAAGAAAGAAAGATGAAAGAGAGAGAGATGTCAGATCCCTCCACCGCAACTTGTCTT 1539

Qy      153 ValCysGluArgAlaGluGlnAspGlnAsnLeuGluValHisValTrpAsnGlnGlu 172
Db      1540 CTTCGAGGTAAAGTCGAGATGAGTGGCCCATCTTAAGCTTACGTCACGAGACAG 1599

Qy      173 GlnAspSerPheTrpValHisHisAspIleLeuLeuSerAlaTrpProLeuSerValGlu 192
Db      1600 GAGGCGCAACCTTTCACGTCACACGATATGCTGCCCGCCATCCCTCTGTGCTTGA 1659

Qy      193 TrpLeuAsnPheAsp-----ProSerProAspAspSerThrGlyAsnTrpIleAla 209
Db      1660 TGGCTGATTTCCCTGTTGGCGCACACACGATGACCGGCAATATTCGTGGCC 1719

Qy      210 ValGlnAsnMetThrProValIleGluValTrpAspLeuAspIleValAspSerLeuGlu 229
Db      1720 GTAGAAACCATGAGCCGACATTTGAGGTCTGGACCTGACATCTTCGATCATATAC 1779

Qy      230 ProValPheThrLeuGly-----SerLysLeuSerLysLys 242
Db      1780 CCAAAACCGCATCTCTGCTCAGGCGGCTGCCGAGCTCGAGGAGACATGAAAGAGCTTAA 1839

Qy      243 LysLeuLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeu 262
Db      1840 AAGTCAAGAGAGACCAAGCGAATGACGATTCACACGTCGACTCGTGTGCTTGCCTTG 1899

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Qy      263 SerTrpAsnLysLeuLeuArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIle 282
Db      1900 GCTGCMAACCGCAACCGCAATCTGTGATCGATCGATCCGCTGATCCGTAATAA 1959

Qy      283 LeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysVal 302
Db      1960 CTCTGGAGCTCAACACCGCCCAAGTGGCCCAATCTTACCAACCATATACGACCAAGGTG 2019

Qy      303 GlnThrLeuGlnPheHisProPheGlnAlaGlnThrLeuLeuSerGlySerTrpAspLys 322
Db      2020 TGCTGCTGACTGAGACCCCTTAAGAGCTTACCGTTCTCTCACCGGTATTCATCTCT 2079

Qy      323 SerValIleLeuTrpAspCysArgSerProAspGluSerHisArgMetTrpArgPheSer 342
Db      2080 ACCGTGTGGCGGCGACATGAGAGCTCCGACCGCAAGAGCCGG--TGGGAGTGGAT 2136

Qy      343 GlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSerThr 362
Db      2137 GCCGAGTCGAGAAATGTGGTGGATTCACGACCAACTTCTTATGTACACACA 2196

Qy      363 AspAspGlyPheValTrpAsnLeuAspAlaArgSer-----Asp 375
Db      2197 GATGCCGTATGTGCTTACCGCTACGATGTCGAACATCTCTGCAACGCCAAAGATCG 2256

Qy      376 LysProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSer 395
Db      2257 AAACGGTGTGACCGCTTGACGCGCATGACACTCTGTCTATCTTGTACATCAACCT 2316

Qy      396 GlnIleLysGlyCysLeuValThrAlaSerAlaAspLysTrpValLysIleTrpAspIle 415
Db      2317 GCCATTCCTGGCTTCCCTTAACCGGATCAAGATCAACCAAGTCAAGCTATGAAACGTC 2376

Qy      416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCys 435
Db      2377 GAGATGGCGGGCTACGATGATGCTCTGCGTACGATGACGATGGTGAAGGTTTTCG 2436

Qy      436 SerSerCysAspProAsp-----LeuProPheIleTrpAlaPheGlyGlyGlnGlu 453
Db      2437 ACCACTTGGCTCTTACACCAAGAGTGGCTTCGCGGTGGAGTGGAGCAAGGA 2496

Qy      454 GlyLeuArgValTrpAspIleSerThrValSerSerValAsnGluAlaPheGlyArgArg 473
Db      2497 ACCGTCAAGATCTGGACACCTCGACCAACGAGCGGTCTGTAGAGCTTTGTGTCTCGC 2556

Qy      474 GlnArgLeuValLeuGlySerAlaArgAsnSerIleSerGlyProPheGlySerArg 493
Db      2557 ATGCCCGCCCTGGAAGCGAGATCAAGAGCGCACATGAGAGTGCAGCCGACGATGAT 2616

Qy      494 SerSerAsp 496
Db      2617 GAATCCGAT 2625

RESULT 9
US-10-128-714-1208
; Sequence 1208, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengli
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshekin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27

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PRIOR APPLICATION NUMBER: US 60/295,890
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/303,899
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US 60/316,362
 PRIOR FILING DATE: 2001-08-31
 NUMBER OF SEQ ID NOS: 8603
 SOFTWARE: Patent version 3.1
 SEQ ID NO 1208
 LENGTH: 1617
 TYPE: DNA
 ORGANISM: Aspergillus fumigatus
 US-10-128-714-1208

Alignment Scores:

Pred. No.:	5 03e-99	Length:	1617
Score:	907.50	Matches:	205
Percent Similarity:	54.97%	Conservative:	88
Best Local Similarity:	38.46%	Mismatches:	188
Query Match:	34.38%	Indels:	53
		Gaps:	10

US-09-315-355c-10 (1-501) x US-10-128-714-1208 (1-1617)

QY 4 SerArgGlnValThrCysValAlaIleArgCysGlyValAlaIleGluThrProAsp 23
 DB 4 TCTTCTATGATCAGTACGACCGCTTGCGTGGCGGGAGTCGCTGCCCAATTCCTACC 63
 QY 24 LysValGluLeuSerLysGluGluValLysArgLeuIleAlaGluAlaLysGluLysLeu 43
 DB 64 AAATATGATGATTCAGAGAGAAATGAAACCGATATCCAACTCGCTCGATCAGCTC 123
 QY 44 GlnGluGluGlyGlySerAspGluGluGluThrGlySerProSerGluAspGlyMet 63
 DB 124 GAAGGCGCCAGGGGATCTGAGGCTGCCAGGAGGAAG--GACCAAGAGCGGAG 180
 QY 64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
 DB 181 ACCATGAGAGAGATCAGAGAGAAAGAACCAAGACCGGATGAGAGAGATTCGAGGAA 240
 QY 84 AspArgThr----- 86
 DB 241 AAGAAGG-AAAAGCAAGTTCAATGAGTAGCTTAAGCTTAAGTCGCGATCTTATA 299
 QY 87 -----LeuAspAspAspGluLeuAlaGluThrAsp 96
 DB 300 TAGACAAGCTTAACACGTCGATCTCGCTTGATGTAAGATTGAAGAAATACGAC 359
 QY 97 LeuAspLysTyrAsp---GluGluGlyAspProAspAlaGlu-----ThrLeuGlyGlu 113
 DB 360 CTTGATCACTACGACAGATGAGAGTGCATGAGATGAGAGAAAGATCACCATCTTCCGA 419
 QY 114 SerLeuGluGlyLeuThrValTyrGlySerAsnAspGlnAspProTyrValThrLeu-- 132
 DB 420 AACGTCAAGTCGCTAGCGTACCAACCAACGAGAGAAATCATATCTGTGATACG 479
 QY 133 LysAspThrGluGluGluGluGluAspLeuIleLysProSerAspAsnLeuIle 152
 DB 480 GAAGAAGAGAGATGAAG 539
 QY 153 ValCysGlyArgAlaGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 172
 DB 540 CTTGCAAGTAAAGTCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
 QY 173 GluAspSerPheTyrValHisHisAspIleLeuLeuSerAlaTyrProLeuSerValGlu 192
 DB 600 GAGGGAACCTTTACGTGACCAACGATTAATGCGCCGCGCCGCTGCTGCTGCTGAA 659
 QY 193 TrpLeuAsnPheAsp-----ProSerProAspAspSerThrGlyAsnTyrIleAla 209
 DB 660 TGGCTGGATTCCTGTTGGGCAACACGATGACCGGATACCGGGAATTTGCTGGCC 719
 QY 210 ValGlyAsnMetThrProValIleGluValTrpAspLeuAspIleValAspSerLeuGlu 229

DB 720 GTAGGAACCATGAGCGCCGACATGAGTGTGGAGACTGGACATTCGACTGCATCTAC 779
 QY 230 ProValPheThrLeuGly-----SerLysLeuSerLysLysLys 242
 DB 780 CCAAGCCCATCTGCTGCTGAGCGCGCTGCGAGCTGAGAGAGACATGAAGAGGCTTAA 839
 QY 243 LysLysLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeu 262
 DB 840 AAGTCCAGAAGAAGAACCAAGGAGATGACAGATTCACAGTCGACCTCGCTCGCTTG 899
 QY 263 SerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIle 282
 DB 900 GCTGCAAAACCCGCAACACCGCAATCTGCTGATGCACTGCACTGCACTGCACTGCA 959
 QY 283 LeuTrpAspSerSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysVal 302
 DB 960 CTCTGGAGCTTCAACACCGCCCAAGTGGCCAAATTTACACCCATCATACGAGCAAGGTG 1019
 QY 303 GlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerTyrAspLys 322
 DB 1020 TGCTCGCTGAGCTGCGACCTTAAGAAAGTACCGCTTCTCTCACCGGATTAAGATCGT 1079
 QY 323 SerValAlaLeuTyrAspCysArgSerProAspGluSerHisArgMetTyrArgPheSer 342
 DB 1080 ACCGTGTGCGGCGACAGATGAGAGCTCCGACGCAAGCGCG--TGCGGAGTGAT 1136
 QY 343 GlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSerThr 362
 DB 1137 GCGGACCTTCAGAAATGCGCGTGGAAATTCACGACCCAAATCTTCTATGTCACCA 1196
 QY 363 AspAspGlyPheValTyrAsnLeuAspAlaArgSer-----Asp 375
 DB 1197 GATGCCGATGATGCTTACCCCTACGATGTTGGAACATCCCTGCAACGCCAAGAAATCG 1256
 QY 376 LysProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSer 395
 DB 1257 AAACCGGTGACACCTGCGAGCGCATGACACCTGTGTCATCTTGCATCAACACCT 1316
 QY 396 GlnIleLysGlyLysLeuValThrAlaSerAlaAspLysTyrValLysIleTrpAspIle 415
 DB 1317 GCCATTCCTGCTCTCTGTAACCGATCAACGATTAACGAAATCAAGTATGAAAGCT 1376
 QY 416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCys 435
 DB 1377 GAGAAAGCGCGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1436
 QY 436 SerSerCysAspProAsp-----LeuProPheIleTyrAlaPheGlyGlnLysGlu 453
 DB 1437 ACACACTTGCCTCTGCAACAGAGTGGCTTCGCTGCGGTGCGGTAGCTGACCAAGGA 1496
 QY 454 GlyLeuArgValTrpAspIleSerThrValSerSerValAsnLysAlaPheGlyArg 473
 DB 1497 ACCGTCCAGTCTGGGACACCTGACCAAGAGAGCGTGTGTAGACTTTGTGCTCGC 1556
 QY 474 GluArgLeuValLeuGlySerAlaArgAsnSerIle 486
 DB 1557 ATGCCCGCCCTGGAAGCGAGTCAAGAGCGCAATC 1595

RESULT 10
 US-09-949-029-59
 Sequence 59. Application US/09949029
 Publication No. US20030134278A1
 GENERAL INFORMATION:
 APPLICANT: Karpen, G.H.
 APPLICANT: Dobie, K.W.
 APPLICANT: Kennedy, C.D.
 APPLICANT: Velasco, V.M.
 APPLICANT: McGrath, T.L.
 APPLICANT: Meko, J.
 APPLICANT: Patterson, R.W.
 TITLE OF INVENTION: Identification of chromosome inheritance modifiers in Drosophila
 TITLE OF INVENTION: melanogaster

DB: 13 Gaps: 22
US-09-315-355c-10 (1-501) x US-10-032-585-6502 (1-1839)
Qy 7 ValThrCysValAlaATPPValArgCysGlyValAlaLysGluThrProAspLysValGlu 26
Db 4 ATTTCTTCAAGTGGTGGTTCAGGAGGGGTTTCTGCTGCAATTCCTCCAGAGAAATATGAA 63
Qy 27 LeuSerLysGluValLysArgLeuLeuAla-----GluAla 39
Db 64 TTAGATGATGAGAAATGAGAAAGATCATCCATGCCATTTAGAACTTAATGATGATGCC 123
Qy 40 LysGluLysLeuGluGluGlyGlyGlySerAspGluGluThrGlySerProSer 59
Db 124 AAAGAACATATTCAGCAGAGCAGAGGT-----GAGAGAGAAACA----- 162
Qy 60 GluAspGlyMetGlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGly 79
Db 163 -----GAGAGCAAT 171
Qy 80 Asp-----ProGluAspAspArgThrLeuAsp-----AspAspGlu 91
Db 172 GATTGGGGAATGCCCAAAACATCTAAATTAAGTGAACAATTTGAATGATGATGAT 231
Qy 92 LeuAlaGluTyraAspLeuAspLysTyraSp--GluGluGlyAspProAspAlaGluThr 110
Db 232 TTAAAGAAATATGATTTAGAAATTAATGATGATGATGATGATGATGATGATGAT 291
Qy 111 LeuGluGluSerLeuLeuGluGlyLeuThrValTyraGlySerAsn----- 124
Db 292 TTAGAAATATCTAAATCTCCATGTTCCAGTTTATCCATTAAGTGAATTAATTA 351
Qy 125 -----AspGlnAspProTyraValThrLeuLysAsp-----ThrGluGln 137
Db 352 CAATGATGAAGTGAAGAGAGTGAATTAATTAATTAATTAATTAATTAATTAATTA 411
Qy 138 TyraGluArgGluAspPheLeuLeuLysProSerAspAsnLeuLeuValCysGlyArgAla 157
Db 412 GAGAGAAAGAAAGAAATCAAAATTTATCACTGATTAATTAATTAATTAATTAATTA 471
Qy 158 GluGluGluGlnCysAsnLeuGluValHisValTyraAsn----- 170
Db 472 GAGAGATATATCTTGGTGGATATTAATTAATTAATTAATTAATTAATTAATTA 531
Qy 171 -----GlnGluGluAsp----- 174
Db 532 GGTCTGAGAGAGAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTA 591
Qy 175 -----SerPheTyraValHisHisAspLeuLeuSerAlaTyraProLeuSerValGlu 192
Db 592 GAATCAAAATTTGATATGATCACCATGATATCAATGATTAATTAATTAATTAATTA 651
Qy 193 ThrLeuAsnPheAspProSerProAspAspSerThr-----GlyAsnTyraLeuAlaValGly 211
Db 652 TGGATTAATTAATTAATCAAGTCAAGAACATCAATATTAATTAATTAATTAATTA 711
Qy 212 AsnMetThrProValLeuGluValTyraAspLeuAspLeuAspSerLeuGluProVal 231
Db 712 ACTTTGACCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 771
Qy 232 PheThrLeuGly-----SerLysLeuSerLys 240
Db 772 GTTATTTTGGGTGAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 831
Qy 241 LysLysLysLysLysGlyLysLysSerSerSerSerSerSerSerSerSerSerSer 260
Db 832 AAAAG 885
Qy 261 AspLeuSerThrPheLysLeuLeuLeuArgAsnValLeuLeuLeuLeuLeuLeuLeu 280
Db 886 TCCTTTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 945
Qy 281 ValLeuLeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeu--AlaValHisThr 299

Db 946 GTGAAATTAATGAGATTTGAACAGTCTACTGCTTTGTTGCTGTTGTAATAATTCATCAT 1005
Qy 300 AspLys-----ValGlnThrLeuGlnPheHisPheProPheGlyValAlaGlnThrLeuLeuSerGly 318
Db 1006 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1065
Qy 319 SerTyraAspLysSerValAlaLeuTyraSpCysArg----- 330
Db 1066 GGGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1125
Qy 331 SerProAspGluSerHisArgMetTrpArgPheSerGly-----GlnLeuGluArgValThr 349
Db 1126 TCATCAGATTTCTTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1185
Qy 350 TrpAsnHisPheSerProCysHisPheLeuAlaSerThrAspAspGlyPheValTyraAsn 369
Db 1186 TGGGATCTTTCTTAACCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1245
Qy 370 LeuAspAlaArgSerAsp--LysProLysPheThrLeuAsnAlaHisAsnAspGluLe 388
Db 1246 TTGATATTCAGACAGAGATTCATTAAGCATTATGATGATGATGATGATGATGAT 1305
Qy 389 SerGlyLeuAspLeuSerSerGlnLeuGlyCysLeuValThr--AlaSerAlaAsp 407
Db 1306 TCTTCATTTGACGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1365
Qy 408 LysTyraValLysLysLeuPhePheLeuGlyLysArg----- 419
Db 1366 AAGATGATCAAACTTTGAGAAATGCCCTTCATCGCTGATGAGAAATTAACACCAACCA 1425
Qy 420 -----ProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCysSerSer 437
Db 1426 CAAGGTCTCTCCATGTTGTTGTCAGAGATTTGTTGTTGTTGTTGTTGTTGTTGTT 1485
Qy 438 CysCysProAspLeuProPheLeu-----TyraLysPheGlyGlyGlnLysGluGlyLeu 455
Db 1486 TATGCTCTCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1545
Qy 456 ArgValTrpAspLysSerThrValSerSerValAsnGluAlaPheGlyArgArgGluArg 475
Db 1546 AAATATGAGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1605
Qy 476 LeuValLeuGlySerAlaArgAsn-----SerSerLeuSer 487
Db 1606 GATTAACAAATATATGCTAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1665
Qy 488 GlyProPheGlySerArgSerSer 495
Db 1666 AGAAATATTAACAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1689

RESULT 12
US-10-320-797-2234
Sequence 2234, Application US/10320797
Publication No. US20040014955A1
GENERAL INFORMATION:
APPLICANT: Zamedio, Carlos
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
FILE REFERENCE: 10182-021-999
CURRENT APPLICATION NUMBER: US/10/320, 797
PRIOR APPLICATION NUMBER: 60/341, 261
NUMBER OF SEQ ID NOS: 3361
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2234
LENGTH: 1638
TYPE: DNA
ORGANISM: Cryptococcus neoformans
US-10-320-797-2234

Search completed: January 31, 2004, 04:36:00
job time : 530 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2004, 03:09:12 ; Search time 100 Seconds
(without alignments)
2211.329 Million cell updates/sec

Title: US-09-315-355C-10

Perfect score: 2640

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LIST=45 -DOCLALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_MMAP -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSFBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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5: /cg2_6/pctdata/2/ina/6C.COMB.seq:*

6: /cg2_6/pctdata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303.5	11.5	696	3	US-08-998-416-1050 Sequence 1050, Ap
2	216	8.2	2314	3	US-08-105-454-1 Sequence 1, Appl
3	205.5	7.8	1929	3	US-08-105-454-9 Sequence 9, Appl
4	200.5	7.6	1211	3	US-09-063-743-2 Sequence 2, Appl
5	200.5	7.3	1211	4	US-09-590-540-2 Sequence 2, Appl
6	191.5	7.3	2119	3	US-09-032-372-6 Sequence 6, Appl
7	190.5	7.2	1738	4	US-09-620-312D-615 Sequence 615, App
8	190.5	7.2	2100	4	US-09-013-118-2 Sequence 2, Appl
9	179	6.8	274	4	US-09-313-284A-1839 Sequence 1839, Ap
10	179	6.8	2481	3	US-08-899-578-1 Sequence 1, Appl
11	179	6.8	43676	3	US-09-356-952-12 Sequence 12, Appl
12	178.5	6.8	1221	3	US-08-965-600-2 Sequence 2, Appl

13	178.5	6.8	1221	4	US-09-489-506-2	Sequence 2, Appl
14	178.5	6.8 <td>2338</td> <td>4<th>US-09-620-312D-411</th><th>Sequence 411, App</th></td>	2338	4 <th>US-09-620-312D-411</th> <th>Sequence 411, App</th>	US-09-620-312D-411	Sequence 411, App
15	173.5	6.6 <td>2272</td> <td>4<th>US-09-108-857-1</th><th>Sequence 1, Appl</th></td>	2272	4 <th>US-09-108-857-1</th> <th>Sequence 1, Appl</th>	US-09-108-857-1	Sequence 1, Appl
16	170.5	6.5	1907	4 <th>US-09-149-476-78</th> <th>Sequence 78, Appl</th>	US-09-149-476-78	Sequence 78, Appl
17	167.5	6.3	2237	4 <th>US-08-914-999-7</th> <th>Sequence 7, Appl</th>	US-08-914-999-7	Sequence 7, Appl
18	167	6.3	2152	1 <th>US-08-188-582-17</th> <th>Sequence 17, Appl</th>	US-08-188-582-17	Sequence 17, Appl
19	167	6.3	2152	1 <th>US-08-646-715-17</th> <th>Sequence 17, Appl</th>	US-08-646-715-17	Sequence 17, Appl
20	165.5	6.3	2359	1 <th>US-08-188-582-4</th> <th>Sequence 4, Appl</th>	US-08-188-582-4	Sequence 4, Appl
21	165.5	6.3	2359	1 <th>US-08-646-715-4</th> <th>Sequence 4, Appl</th>	US-08-646-715-4	Sequence 4, Appl
22	165	6.2	1368	3 <th>US-08-707-399E-1</th> <th>Sequence 3, Appl</th>	US-08-707-399E-1	Sequence 3, Appl
23	164	6.2	1020	3 <th>US-08-707-399E-3</th> <th>Sequence 3, Appl</th>	US-08-707-399E-3	Sequence 3, Appl
24	164	6.2	2085	2 <th>US-08-283-917-8</th> <th>Sequence 8, Appl</th>	US-08-283-917-8	Sequence 8, Appl
25	164	6.2	2085	2 <th>US-08-961-716-8</th> <th>Sequence 8, Appl</th>	US-08-961-716-8	Sequence 8, Appl
26	160	6.1	1841	4 <th>US-09-620-312D-636</th> <th>Sequence 636, App</th>	US-09-620-312D-636	Sequence 636, App
27	159	6.0	7518	4 <th>US-09-620-312D-1051</th> <th>Sequence 1051, Ap</th>	US-09-620-312D-1051	Sequence 1051, Ap
28	158	6.0	1611	4 <th>US-09-302-769-13</th> <th>Sequence 13, Appl</th>	US-09-302-769-13	Sequence 13, Appl
29	156.5	5.9	1517	3 <th>US-09-180-783-1</th> <th>Sequence 1, Appl</th>	US-09-180-783-1	Sequence 1, Appl
30	155.5	5.9	3465	4 <th>US-08-914-999-5</th> <th>Sequence 5, Appl</th>	US-08-914-999-5	Sequence 5, Appl
31	155	5.9	1366	4 <th>US-09-620-312D-867</th> <th>Sequence 867, App</th>	US-09-620-312D-867	Sequence 867, App
32	154.5	5.9	1767	3 <th>US-08-988-856B-1</th> <th>Sequence 1, Appl</th>	US-08-988-856B-1	Sequence 1, Appl
33	154.5	5.9	1767	5 <th>PCT-US95-01806-1</th> <th>Sequence 1, Appl</th>	PCT-US95-01806-1	Sequence 1, Appl
34	153	5.8	2363	4 <th>US-09-620-312D-222</th> <th>Sequence 222, App</th>	US-09-620-312D-222	Sequence 222, App
35	151	5.7	1858	2 <th>US-08-909-965C-11</th> <th>Sequence 11, Appl</th>	US-08-909-965C-11	Sequence 11, Appl
36	150.5	5.7	3067	4 <th>US-09-016-434-1285</th> <th>Sequence 1285, Ap</th>	US-09-016-434-1285	Sequence 1285, Ap
37	149.5	5.7	1700	3 <th>US-08-988-856B-3</th> <th>Sequence 3, Appl</th>	US-08-988-856B-3	Sequence 3, Appl
38	149.5	5.7	1700	5 <th>PCT-US95-01806-3</th> <th>Sequence 3, Appl</th>	PCT-US95-01806-3	Sequence 3, Appl
39	147	5.6	1563	3 <th>US-09-177-249-3</th> <th>Sequence 3, Appl</th>	US-09-177-249-3	Sequence 3, Appl
40	146.5	5.5	1246	4 <th>US-09-302-769-22</th> <th>Sequence 22, Appl</th>	US-09-302-769-22	Sequence 22, Appl
41	145.5	5.5	1394	3 <th>US-09-147-826B-1</th> <th>Sequence 1, Appl</th>	US-09-147-826B-1	Sequence 1, Appl
42	145	5.5	2186	4 <th>US-09-184-001-1</th> <th>Sequence 1, Appl</th>	US-09-184-001-1	Sequence 1, Appl
43	145	5.5	2558	4 <th>US-09-184-001-3</th> <th>Sequence 3, Appl</th>	US-09-184-001-3	Sequence 3, Appl
44	144.5	5.5	1115	1 <th>US-08-190-802A-19</th> <th>Sequence 19, Appl</th>	US-08-190-802A-19	Sequence 19, Appl
45	144.5	5.5	1115	3 <th>US-08-477-346-19</th> <th>Sequence 19, Appl</th>	US-08-477-346-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-998-416-1050
Sequence 1050, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998.416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CCG1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1050:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1640UP
US-09-998-416-1050

Alignment Scores:
Pred. No.: 2,16e-24 Length: 696
Score: 303.50 Matches: 87
Percent Similarity: 45.88% Conservative: 30
Best Local Similarity: 34.12% Mismatches: 71
Query Match: 11.50% Indels: 68
DB: 3 Gaps: 8

US-09-315-355c-10 (1-501) x US-08-998-416-1050 (1-696)

Qy 31 GluValIysArgLeuIleAlaGluAlaLysGluLysLeuGluGluGlyGlySer 50
Db 8 GAGCTGGGGCGGAGCTGACCTGACGATGCGAGAGAGGCGCTGAGAGAGCGCGGTGGCG 67
Qy 51 AspGluGluGluThrGlySerProSerGluAspGlyMetGlnSerAlaArgThrGlnAla 70
Db 68 CAGAGGGCGCGGGCGCTGGCGCGCAATTGACCGT----- 103
Qy 71 ArgProArgGluProLeuGluAspGlyAspProGluAspAspArgThrLeuAspAspAsp 90
Db 104 -----GACGAC 109
Qy 91 GluLeuAlaGluIlyrAspLeuAspLysIlyrAspGluGlu-----GlyAspProAspAla 108
Db 110 GACCTGAAAGAGAGTACGACTTGAGACACTACAGAGAGAGGATGCGGGCGCGGTGCAGAG 169
Qy 109 GluThrLeuGlyGluSerLeuLeuGlyLeuThrValTyr-----GlySerAsnAspGln 126
Db 170 GTGACGATGTTCCCGGGGCTCTCGGGCGAGCGGCGCTTCCACGAGGGGTGAGAGGGGAG 229
Qy 127 AspProIlyrValThrLeuLys-----AspThrGluGlnTyrGluArgGluAspPheLeu 144
Db 230 GACCGGTACCTGAGCTTCCAAACCGTAGAGAGAGGAGCGGCGGCGGACCTGCAG 289
Qy 145 IleLysProSerAspAsnLeuIleValCysGlyArgAlaGluGluAspGlnCysAsnLeu 164
Db 290 GTGATCCCGACAGACACCTGCTGTGCAACGCGAGCGAGACGACATTTCGTACTTG 349
Qy 165 GluValHisValIlyrAsn----- 170
Db 350 GACGTGACGTGACGACGAGCGCGGGGTTCCACAGACGAGGGGGTCCCGCAGAGGCC 409
Qy 171 -----GluGluGluAsp-----SerPheTyrVal 178
Db 410 GGGGACGGCGAGACCCCGACGTGGCGCGCGCTGATACGAGACGCTCTTGTACTGTG 469
Qy 179 HisHisAspIleLeuLeuSerAlaTyrProLeuSerValGluTyrLeuAsnPheAspPro 198
Db 470 CACACGACGTGATGTTCCGCACTTCCGCTGTGCGGTGAGTGGTAACTACCGCGCC 529
Qy 199 ---SerProAspAspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIle 217
Db 530 GGGGTGAACCTGACGCGCGCGCAAACTTTGCGGGGTGCGGACCTTCAGACCCACAGATC 589
Qy 218 GluValTyrAspLeuAspIleValAspSerLeuGluProValPheThrLeuGly----- 235
Db 590 GAGCTGTGAACCTGACCTGTGTGACCGCGCGTCCCGAC-ATGATCTCTCGGCGAGGCC 648

Qy 236 -----SerLysLeuSerLysLysLysLys 244
Db 649 GCGGACTCTGCGACCGCGTCCAGAGAGTCAAGAGAGAGAGAG 693

RESULT 2
US-08-105-454-1
Sequence 1, Application US/08105454
Patent No. 6071715
GENERAL INFORMATION:
APPLICANT: Qian, Yue-Wei
TITLE OF INVENTION: No. 6071715el Proteins Which Bind to
TITLE OF INVENTION: Retinoblastoma Proteins and Their
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 2300 One American Center
CITY: Austin
STATE: TX
COUNTRY: USA
ZIP: 78701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,454
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kirchell, Barbara
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: US/K:196/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 85..1362
US-08-105-454-1

Alignment Scores:
Pred. No.: 7.9e-14 Length: 2314
Score: 216.00 Matches: 84
Percent Similarity: 35.97% Conservative: 66
Best Local Similarity: 20.14% Mismatches: 133
Query Match: 8.18% Indels: 134
DB: 3 Gaps: 13

US-09-315-355c-10 (1-501) x US-08-105-454-1 (1-2314)

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Qy 101 AspGluGluGlyAspProAspAlaGluThrLeuGlyGluSerLeuLeuGlyLeuThrVal 120
Db 379 GACAGTAG-----AAAGAGAA-----TTTGAGGT 405
Qy 121 TyrGlySerAsnAspGluAspProIlyrValThrLeuLysAspThrGluGlnTyrGluArg 140
Db 406 TTGGTTCAGTTAGTGAGAAAAATTGAATGAATCAAGATCAACATGAAGAGAGATA 465

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QY 141 GluAspPheLeuIleYsProSerAspAsnLeuIleValCysGlyAlaGluGlnAsp 160
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QY 161 -----GlnCys 162
Db 526 GATGTTCTGCTTGTGACTATACAAAACATCCTTAACACAGATCCTTGTGAGAGAGC 585
QY 163 AsnLeuGluValHisValTyrAsnGlnGluAspSerPheTyrValHisAspIle 182
Db 586 AACCCAGACTGCGCTCCCGGACATCAGAAAGAGAGCTTGGCTTCTTGGAACCCA 645
QY 183 LeuLeuSerAlaTyrProLeuSerValGluTyrLeuAsnPheAspProSerProAsp 202
Db 646 AATCTCAGTGGGACCTTACTTAGT-----GCTTCAGATGAC 681
QY 203 SerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGluValThrAspLeu 222
Db 682 CATACC-----ATCTGCGCTGGGACATC 705
QY 223 AspIleValAspSerLeuGluProValPheThrLeuGlySerTyrLeuSerTyrLeu 242
Db 706 AGTCCCGTT----- 714
QY 243 LysLysLysGlyLys-----LysSerSerSerAlaGluGlyHisThrAspAlaVal 259
Db 715 CCAAGAGAGGAGAAAGGTAGATCCGAAAGACCATCTTACAGGCGCATAGCGAGTAGTA 774
QY 260 LeuAspLeuSerThrPheAsnLeuIleArgAsnValLeuAlaSerAlaSerAlaAsp 279
Db 775 GAAAGATGTTCTCGTCACTACTCATGATGATGCTGTTGGGTGATGATGATGATG 834
QY 280 ThrValIleLeuTyrAspMet-----SerLeuGlyLysProAlaSerIleVal 296
Db 835 AAACCTTAGATTTGGGATACCTGTTCAACAACATCTTCAACCAAGCCACTGATAT 894
QY 297 ValHisThrAspLysValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeu 316
Db 895 GCTCACACTGCGTGAAGTACGCGCTTCTTCAATCTTATAGAGATTCATCTTCC 954
QY 317 SerGlySerTyrAspLysSerValAlaLeuTyrAspCysArgSerProAspGluSer 336
Db 955 ACAGGATGACGTGACAAAGCTGCTGCTGAGATGACGAG----- 996
QY 337 ArgMetThrArgPheSerGlyGlnIleGluArgValThrThrAsnHisPheSerPro 356
Db 996 ----- 996
QY 357 HisPheLeuAlaSerThrAspAspGlyPheValTyrAsnLeuAspAlaArgSerAsp 376
Db 997 -----AATCGAAACTTAG----- 1011
QY 377 ProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerGln 396
Db 1012 ---TTGCAATCTCTTGAAGTACATAGATGAATATTCAGAGTTCAGTGCATCCTCAC 1068
QY 397 IleLysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleThrAspIle 415
Db 1069 AATGAGACTATTATTGCTTCCAGTGTACTGATCCCAAGCTGAATGTGGAGTTTAGT 1128
QY 416 ---LeuGlyAspArgProSerLeuValHisSerAlaGlyAspMetLysMetGlyValLeu 434
Db 1129 AAAATTTGAGAGAACCAATCCCAAGATGACAGAGAGGAGCCACAGAGTTGTTT 1188
QY 435 CysSer-----SerCysCysProAspLeuProPhe 444
Db 1189 ATTCAATGATGATCATGCTGCAAGATATCTGATTTCTCTGGAATCCCAATGAACCTTGG 1248
QY 445 IleTyrAlaPheGlyGlyGlnLysGluGlyLeuArgValThrAspIleSer 461
Db 1249 GTGATTTGTTCTGTATCAGAAAGCAATATCATGCAAGTGTGGCAATGGCA 1299

```

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US-08-105-454-9
; Sequence 9, Application US/08105454
; Patent No. 6071715
; GENERAL INFORMATION:
; APPLICANT: Qian, Yue-Wei
; APPLICANT: Lee, Eva Y.-H. P.
; TITLE OF INVENTION: No. 6071715el Proteins which Bind to
; TITLE OF INVENTION: Retinoblastoma Proteins and Their
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 2300 One American Center
; CITY: Austin
; STATE: TX
; COUNTRY: USA
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,454
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: USK:196/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1929 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-105-454-9
;
; Alignment Scores:
; Pred. No.: 8.68e-13 Length: 1929
; Score: 205.50 Matches: 71
; Percent Similarity: 38.36% Conservative: 69
; Best Local Similarity: 19.45% Mismatches: 102
; Query Match: 7.78% Indels: 123
; Gaps: 12
;
; US-09-315-355c-10 (1-501) x US-08-105-454-9 (1-1929)
QY 126 GlnAspProGlyValThrLeuLysAspThrGluGlnTyrGluArgGluAspPheLeuIle 145
Db 661 CAGATCTCATCATCATCTGCTACAAAACA----- 690
QY 146 LysProSerAspAsnLeuIleValCysGlyArgAlaGlu----- 158
Db 691 ---CCATCTTCTGATGAGTGGTGGTTTGTGACTATACAAAACCCCTGTAACAGACCCA 747
QY 159 GlnAspGlnCysAsnLeuGluValHisValTyrAsnGlnGluAspSerPheTyrVal 178
Db 748 AGTGAAGAAATATATCTGATCTCAGATTTAAGAGTCAACAGAAAGAGCTATGCTC 807
QY 179 HisHisAspIleLeuLeuSerAlaTyrProLeuSerValGluTyrLeuAsnPheAsp 198
Db 808 TCTCGAATTCAAATTTGAGTGGACATCTCTTAAGT----- 843
QY 199 SerProAspAspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGlu 218
Db 844 GCATCTATATGACCTACT-----GTTTGT 867
QY 219 ValThrAspLeuAsp-----IleValAspSerLeuGluProVal 231

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Db      868 CTGTGGGATTATTAACGCAGAACCAAAAAGAAGCAAATAATTGGAGTCT---AAGGCATC   924
           |||||.....|||.....:::..:::
Oy      232 PheThrLeuGlySerLysLeuSerLysLysLysLysLysLysLysSerSerSer 251
           |||||
Db      925 TTTACT-----930
Oy      252 AlaGluGlyHisThrAspAlaValLeuAsnLeuSerTrpAsnLysLeuIleArgAsnVal 271
           |||||.....|||.....:::~::~:
Db      931 -----GGCCATCATCGCTGTGTAAAGAGATGGGCTGGCACCTGCTCCAGCATCTTG 984
Oy      272 LeuAlaSerAlaSerAlaAspAsnThrValIleLeuTrpAspMet-----SerLeu 288
           |||.....|||.....:::~::~:
Db      985 TTGGATCTGTTCCTGGATGATACGAACCTTATGATATGGACACCAGSTCCAAATTCACC 1044
Oy      289 GlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeuGlnPheHis 308
           |||||.....:::~::~:
Db      1045 TCCAAGCCGAGCATCTGTGGATGCGACACTGCCGAAGTCACATCGCTCTCATTTCAAT 1104
Oy      309 ProPheGluAlaGlnThrLeuIleSerGlySerTyraAspLysSerValAlaLeuTyrrsp 328
           |||||.....:::~::~:
Db      1105 CCTTACACCGCAATTTATTTCTAGCCCAAGGCTCTGGGATTAAGACCGTGGCTTTTAGGAT 1164
Oy      329 CysArgSerProAspGluSerHisArgMetTrpArgPheSerGlyGlnIleGluArgVal 348
           |||
Db      1165 CTGGCT-----1170
Oy      349 ThrTrpAsnHisPheSerProCysHisPheLeuAlaSerThrAspAspGlyPheValTyr 368
           |||||
Db      1170 -----1170
Oy      369 AsnLeuAspAlaArgSerAspLysProIlePheThrLeuAsnAlaHisAsnAspGluIle 388
           |||||.....:::~::~:
Db      1171 AACTTAAATATTAATA--CTCATACCTTCGATTCATTAAGATGAATTT 1218
Oy      389 SerGlyLeuAspLysSerSerClnIleLysGlyCysLeuValThrAlaSerAlaAspLys 408
           |||.....|||.....:::~::~:
Db      1219 TTCACAGGTCCACTGCTCCACATATATGAACAATATTCTGGCTTCAAGTGAATCAGCCG 1278
Oy      409 TyrValLysIleTrpAspIle-----LeuGlyAspArgProSerLeuValHisSerArg 426
           :::~::~:
Db      1279 CGCCTGAATGTGTGATTTAAGTAAATTTGGGANAAGAACATATCAGCAAGATGCACAA 1338
Oy      427 AspMetLysMetGlyValLeuPheCysSer-----436
           |||||.....:::~::~:
Db      1339 GATGGCCCTCCAGAACTCTCTGTTTATTCATGAGAGACACACTGCTAAGATTTCAGATTTT 1398
Oy      437 SerCysCysProAspLeuProPheIleTyrAlaPheGlyGlyGlnLysGluGlyLeuArg 456
           |||||.....:::~::~:
Db      1399 AGCTGGAAACCCCAAGACCTTGGGTCAATTGCTCAGTCTGAGGATTAACATCATCTGAG 1458
Oy      457 ValTrpAspIleSer 461
           :::~::~:
Db      1459 ATATGGCAAAATGCT 1473

RESULT 4
US-09-06:-743-2
; Sequence 2, Application US/09063743
; Patent No. 6242214
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

```

[illegible]

QY 342 SerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSer 361
DB 628 ACATACAGAGGTGTTAGCTGACCTTCAATGACACAGATGAT---CAGATTATTTCTGGT 684
QY 362 ThrAspArgGlyPheValTyrAsnLeuAspAlaArgSerArgProIlePheThrLeu 381
DB 685 GGAATTAACATGATATTCAGTGTGGACCTGGCCAGAACAAAGCTTAACCTACACCATG 744
QY 382 AsnAlaHisAsnAspGlnIleSerGlyLeuAspLeuSerSerGlnIleGlyCysLeu 401
DB 745 AGAGGCATGACATTCAGTACCTGCTGCTTAACTTCTGAA---GGCTTTATCTT 801
QY 402 ValThrAlaSerAlaAspLysTyrValIleTyrAspIleLeuGlyAspArgProSer 421
DB 802 TTGTTCATGCAATGACAAATACATGCTGTCTGGGATGTC-----CGGCATTT 852
QY 422 LeuValHisSerAlaArgAspMetLysMet-----Gly 431
DB 853 GCCCCCAAGAGATGTGTAAAGATATTTCAAGAAATGTGCAAACTTTGAAAGAAC 912
QY 432 ValLeuPheCysSerSerCysCysProAspLeuProPheIleTyrAlaPheGlyGln 451
DB 913 CTCTGAGATGTT---TCTTGTCTACCTGATGAAAGCAAAATA---GACGCTGCTCAGCC 966
QY 452 LysGlnGlyLeuArgValTrpAspIleSerThr----- 462
DB 967 GACAGGTTTGTATTGTGTGGATACCAACAGCAGAGAAATATTGTATAAGCTGCCGCC 1026
QY 463 ---ValSerSerValAsnGlu---AlaPheGlyArgGluArgLeuValLeuGlySer 480
DB 1027 CATGCTGCTCCATCAATGAAGTGGCTTTCCACCCTGAGCCCATCATTTATCTCAGCA 1086
QY 481 AlaArgAsnSerSerIle 486
DB 1087 TCGAGTACAGAGACATG 1104

RESULT 5
US-09-590-540-2
Sequence 2, Application US/09590540
Patent No. 6410267
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Guegler, Karl J.
Corley, Neil C.
Patterson, Chandra
TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Genomics, Inc.
STREET: 3160 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/590,540
FILING DATE: 08-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/063,743
FILING DATE: April 21, 1998
ATTORNEY/AGENT INFORMATION:
NAME: David G. Streeter
REGISTRATION NUMBER: 43,168
REFERENCE/DOCKET NUMBER: PF-0508-1 DIV
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGNOT01
CLONE: 059953
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-590-540-2
Alignment Scores:
Score: 1.48e-12 Length: 1211
Percent Similarity: 200.50 Matches: 82
Best Local Similarity: 43.56% Conservative: 60
Query Match: 25.15% Mismatches: 129
Gaps: 7.59% Indels: 55
DB: 4 Gaps: 13

US-09-315-355c-10 (1-501) x US-09-590-540-2 (1-1211)

QY 182 IleLeuLeuSerAlaTyrProLeuSerValGluTrpLeuAsnPheAspProSerProAsp 201
DB 229 ATGCTGTCTCTGTGACATGAAGGAGAGTCTACTGCTGCAAGTTCCACCAC----- 282
QY 202 AspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGluValTrpAsp 221
DB 283 -----GGATCCACTTATGACATCTGCAGGATTTGACCGCATGATATTACTGTG--- 330
QY 222 LeuAspIleValAspSerLeuGluProValPheThrLeuGlySerLysLeuSerLys 241
DB 331 ---AATGCTATGCTGACCTGTGATTAATGCTCCACTG----- 366
QY 242 LysLysLysGlyGlyLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAsp 261
DB 367 -----AAGGACACAGCTGAGCATATGAA 393
QY 262 LeuSerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaAspAsnThrVal 281
DB 394 TTGCATTACAAAC---ACAGATGGCAGATGCTTTCTCAGATCCACAGATAAACCCTG 450
QY 282 IleLeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLys 301
DB 451 GCTGTGTGGATGATGAAACAGGTGAAGGGTTAAAGGCTAAAGGACATTAATCTCTT 510
QY 302 ValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerTyrAsp 321
DB 511 GTGAATTCCTGTTATCCAGCCAGAGAGCCCTGACTGTCTGACATGCGAGGAGAT 570
QY 322 LysSerValAlaLeuTyrAspCysArgSerProAspLeuSerHisArgMetTrpArgPhe 341
DB 571 GGCACAGGTAACTTTGGAGATCCGGAAG---AAACAGCCATCCAGACATTTCAAGAC 627
QY 342 SerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSer 361
DB 628 ACATACAGAGGTGTTAGCTGACCTTCAATGACACAGATGAT---CAGATTATTTCTGGT 684
QY 362 ThrAspArgGlyPheValTyrAsnLeuAspAlaArgSerArgProIlePheThrLeu 381
DB 685 GGAATTAACATGATATTCAGTGTGGACCTGGCCAGAACAAAGCTTAACCTACACCATG 744
QY 382 AsnAlaHisAsnAspGlnIleSerGlyLeuAspLeuSerSerGlnIleGlyCysLeu 401
DB 745 AGAGGCATGACATTCAGTACCTGCTGCTTAACTTCTGAA---GGCTTTATCTT 801
QY 402 ValThrAlaSerAlaAspLysTyrValIleTyrAspIleLeuGlyAspArgProSer 421
DB 802 TTGTTCATGCAATGACAAATACATGCTGTCTGGGATGTC-----CGGCATTT 852

QY 422 LeuValHisSerArgMetLeuMet-----Gly 431
 Db 853 GCGCCCAAGAGCATGTGTAAAGATATTTCAGGAATGTGCACAACTTTGAAAGAAC 912
 QY 432 ValLeuPheCysSerSerCysCysProAspLeuProHeHeIleTyrAlaPheGlyGln 451
 Db 913 CTTCTGAGATGT---TCTGTGTACCTGATGAAACAAATA---GAGCTGCTCAGCC 966
 QY 452 LysGluGlyLeuValTyrAspIleSerThr----- 462
 Db 967 GACAGGTTTGTATTGTGTGGATATCCACAGCAGGAATATTGTATAGCTCCCGGC 1026
 QY 463 ---ValSerSerValaAnglu---AlaPheGlyArgArgGluArgLeuValLeuGlySer 480
 Db 1027 CATGCTGCTTCATCAATGAAGTGCTTTCCACCCTGATGAGCCCATCATATCTCAGCA 1086
 QY 481 AlaArgAsnSerSerIle 486
 Db 1087 TCGAGTGACAGAGACTG 1104

RESULT 6
 US-09-032-372-6
 Sequence 6, Application US/09032372
 Patent No. 6008337
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Guejler, Karl J.
 APPLICANT: Yue, Henry
 APPLICANT: Lal, Preeti
 TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/032.372
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0478 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2119 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: SYNORAB01
 C clone: 78191
 US-09-032-372-6

Alignment Scores: 3.63e-11 Length: 2119
 Pred. No.: Alignment Scores: 3.63e-11 Length: 2119

Score: 191.50 Matches: 101
 Percent Similarity: 35.27% Conservative: 63
 Best Local Similarity: 21.72% Mismatches: 179
 Query Match: 7.25% Indels: 122
 DB: 3 Gaps: 20

US-09-315-355c-10 (1-501) x US-09-032-372-6 (1-2119)

QY 42 LysLeuGlnGluGlyGlySerAspGlu-----GluThrGly 56
 Db 120 CAATATGAGTGCATCTTAGAGATCCCTTCAGAGCTCCGCTTCCTCCTCGCTGCG 179
 QY 57 SerProSerGluAspGlyMetGlnSerAlaArg-----ThrGln 69
 Db 180 TCCCGCGCAAGATGGCAACCGAGGGCTGCACAGAAACGAGACCTGCGCTGTGA 239
 QY 70 AlaArgProArgGluProLeuGluAspGlyAspPro-GluAspAspArgThrLeuAspAs 89
 Db 240 GAGCGAGCGCGAGAGCT-----CAAGGCAAGCTGGAGAGAGAGCGAGCC----- 285
 QY 89 PAspGluLeuAlaGluTyrAspLeuAspIleTyrAspGluGluGlyAspProAspAlaG 109
 Db 286 ---AACCTCAGCATGTGAGCTGCACAGTGGCGAGCGG-----GTGCA 329
 QY 109 uThrLeuGlyGluSerLeuLeuGlyLeuThrValTyrGlySerAsnAspGlnAspProTy 129
 Db 330 GGCCTGGGGCAGTTGTCTATG----- 351
 QY 129 ValThrLeuLysAspThrGluGlnTyrGluAspGluAspPheLeuIleAspProSerAs 149
 Db 352 -----AAGACCAGAAAGACCTCAAGGCCACCG 380
 QY 149 PAsnLeuIleValCysGlyYArgAlaGluGlnAspGlnCysAsnLeuGluValIleValTy 169
 Db 381 GAACAAAGTCTCTGC-----ATGACTGTGTCAAGATTAAGAGAGATCGT 428
 QY 169 rAsnGlnGluLysAspSerPheTyrValHisAspIleLeuLeuSer----- 185
 Db 429 GAGCTGCTCAGACATGGAGAGGTGATCGTGGATTCCTTCCACCAACAAAGAGCA 488
 QY 186 -AlaTyrProLeuSerValGluTyrPleu-----AsnPheAspProSerProAspAs 202
 Db 489 CGGGTCACCATCCCTGCACCGGTGATGATGATGCTTATGCCCATCG----- 540
 QY 202 pSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGluValTyrAspLe 222
 Db 541 -----GATGTGCCATTCCTGTGTGTGTGATATTAAGTGTCTGTATACCCCTT 553
 QY 222 uAspIleValAspSerLeuGluProValPheThrLeuGlySerLysLeuSerLysIleTy 242
 Db 594 G-----ACGTTGACAAAATGAATAACATGCTGCCAAAAA 629
 QY 242 GlyGlyLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLe 262
 Db 630 GAAG-----TCTGTGTATGCAACCACTACCTGTGCGCTG 668
 QY 262 uSerThrAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIle 282
 Db 669 CAGCTTCACCACTGACATGCAATCTG--ACAGCAGCGGCGATGACATCTGC 725
 QY 282 eLeuTyrAspMetSerLeuGlyLysProAlaAlaSerLeuValIleHisThrAspLysVa 302
 Db 726 CCTGTGGAGATGGAGAGCGGCGAGCTGCAGAGCTTCACAGCATGGGCTGAGCT 785
 QY 302 LglnThrLeuGlnPheHisProPheGlu---AlaGlnThrLeuIleSerGlySerTyrAs 321
 Db 786 CCTCTGCTTGACCTGCGCCCTCAGAAACTGGAAACACCTGTGTCTGGGAGATGTGA 845
 QY 321 PysSerValAlaLeuTyrAspCysArgSerProAspGluSerHisArgMetTyrArgPh 341
 Db 846 CAAGAAAGCATGTGTGGACATGCGC----- 873
 QY 341 eSerGlyGlnIleGluArgValThrTyrAsnHisPheSerProCysHis----- 357


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Db      874 -TCGGCGAGTGGCTGAGGCTTTGAAACATGAAATCGACATCAACAGTCCGTA 932
Qy      358 -----PheleuAlaserThraspApbGlyPheValYtrAsnLeuAs 371
Db      933 CTACCCAGTGAAGAGTCCCTTGTCTCAGAGTCAAGCTACGTCGCTTATGA 992
Qy      371 PALATGSeAspLyseProIlePheThLeuAsnAlaHisAsnAspGluIleSerGlyLe 391
Db      993 CTGCGGCGAGATAGGAGAGTGGCATCTATTCAAAAGAAAGCATATTTGGAGATC 1052
Qy      391 waSpLeuSeSerGlnIleYsglyCysLeuValThrAlaSerAlaAspLyseYr--Va 410
Db      1053 CACGCTGAGCTTCTCCCTCAGTGGTCCGCTGCTTTGGATACATATTAACATAT 1112
Qy      410 LysIleTrpAspIleLeu---GlyAspArgProSerLeuValHisSerArgAspMetly 429
Db      1113 CAACGTCGGATGTTCTCAAAAGGATCCGAGTCTCCATCTTTGGACATGAAAACG 1172
Qy      429 smet-----GlyValIleuPheCysSeSerCysCysProAs 441
Db      1173 CGTTAGACACTACGAGCTTCCCGCATGGAGCTGCTTCTGCTCT----- 1218
Qy      441 pleuProPheIleTyrAlaPheGlyGlyGlyGlyGlyLeuArgValIleTrpAspIleSe 461
Db      1219 -----GGATCATGGAGATCATACCTCAGAGCTCGGCGCTAATC 1256
Qy      461 rThrValSerSer 465
Db      1257 ATCTTCTGACAGT 1269
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RESULT 7

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US-09-620-312D-615
; Sequence 615, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungding
; APPLICANT: Wang, Dunru
; APPLICANT: John Tillinghast
; APPLICANT: Dimanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ. ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 615
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(1467)
US-09-620-312D-615
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Alignment Scores:
Pred. No.: 3,42e-11 Length: 1738
Score: 190.50 Matches: 91
Percent Similarity: 34.52% Conservative: 55
Best Local Similarity: 21.51% Mismatches: 138
Query Match: 7.22% Indels: 139
DB: 4 Gaps: 17

US-09-315-355c-10 (1-501) x US-09-620-312D-615 (1-1738)
Qy      132 LeuLysAspThrIleGlnIleTyrGluArgGlu-----AspPheLeuIlelys----- 146
Db      316 CTAAAGACAAAATATAGATTCACAAACATGTGAGATTGATTTCTTTATTAAGGCCAG 375
Qy      147 -----ProSerAspLeuIleValIleCysGlyArgGluGluIleAspGlnCys 162
Db      376 TTTCTCGGAATGCCCTTGGACAAA-----CACATGAAATGGAGAACATC 420
Qy      163 AsnLeuGlu-----ValHisValTyrAsnGlnGluIleAspSer 175
Db      421 TCATCAGAAAGAGTGTGAAATAGAAATAGTGAAGATATCTGACCCCGCAGAG 480
Qy      176 PheTyrValHisAspIleLeuLeuSerAlaTyrProLeuSerValGluTrpLeuAsn 195
Db      481 CAATGCATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 534
Qy      196 PheAspProSerProAspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrPro 215
Db      535 -----ATCTGACTGCTGTTCTTATGATAG 558
Qy      216 ValIleGluValIleTrpAspLeuAspIleValAspSerLeuGluProValPheThrLeuGly 235
Db      559 ACTTTCGGATTCGTCGCTTGGAA----- 582
Qy      236 SerLysLeuSerLysLysLysLysLysGlyLysLysSerSerSerAlaGluGlyHis 255
Db      583 -----GGAAGATCATATATGATGATGATGATGATGATGATGATGATGATGATGATG 612
Qy      256 ThrAspAlaValLeuAspLeuSerThrAsnLys-----LeuIleArgAsnValLeuAla 273
Db      613 ACGGATGTTGTAAGATGAGTGGCTGGTGAAGAAAGATGATGTTGCTGCTTATTTTG 672
Qy      274 SerAlaSerAlaAspSerThrValIleLeuTrpAspMetSerLeuGlyLysProAlaAla 293
Db      673 AGTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714
Qy      294 SerLeuAlaValHisThrAspLysValGlnThrLeu-----GlnPheHisProPhe 310
Db      715 -----GTAGAGAGAAACAAAGTGAAGAGCCCTACATGCTGTAGAGGCTGATGGA 765
Qy      311 GluAlaGlnThrLeu-----IleSerGlySerTyrAsp 321
Db      766 AGTGTAGATTCTATACCTGTTGATGGCTCAGAACTAAATTTTGACATGCTCTGGAT 825
Qy      322 LysSerValAlaLeuTyrAspCysArgSerProAspGluSerHisArgMetTrpArgPhe 341
Db      826 AAGATGCTAAAGATCTGCTGTACAGTCCCTACAGATGAAGAATATAAG----- 876
Qy      342 SerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSer 361
Db      877 -----CAGAGATCCACA----- 888
Qy      362 ThrAspAspGlyPheValTyrAsnLeuAspAlaArgSerAspLys----- 376
Db      889 -----AATGACCAAGAAAGAAACAGAAACAGAAACAGTTGGGA 927
Qy      377 -----ProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAsp 392
Db      928 CTAAACAAGACTCCCATAGTACCTCTCTGGCCACATGAGCAGATTCTCTAGTTCTG 987
Qy      393 LeuSerSerGlnIleYsglyCysLeuValThrAlaSerAlaAspLyseYrValLysIle 412
Db      988 TGGTCAGATGCTGAAGAAATCTGC-----AGTGCATCTTGGAGCATACATTAAGTGT 1041
```

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Qy      413  TrrpshleuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyVal 432
Db      1042  TGGAGTGTGAGTCTGGCAGCTTAAAGCACTTGAACAAGAAATAAAGTTAAATTG 1101
Qy      433  LeuphCySerSerCyCyAspProAspLeuProPheIleTyrAlaPheGlyGlyGlnLys 452
Db      1102  ATTTCCTATCTCCACCTTGTAAACGTTA-----GCATCTGAAGACACAGAT 1149
Qy      453  GluGlyLeuAlaValTrrpAspLleSerThr----- 462
Db      1150  AGGCATATCAGACTGTGGGATCCCGAAGTAAGATGTTCTTGCTGTCCTGCTCCTA 1209
Qy      463  -----ValSerSerValAsnGluAlaPheGlyArgArgGluArgLeu 476
Db      1210  ACGTCACACTACTGTTGGGTGATCAGTCACTAAATAGTCTCCATCCCAAGAACAGACGCTG 1266
Qy      477  ValLeuGlySerAlaArgAsnSerSerLleSerGlyProPheGlySerArgSerSerAsp 496
Db      1270  ATTTCAGAGATCTTTAGATTAAC-----ATTGTTAAGCTGTGGGATACAAAGATTGTAAAG 1323
Qy      497  ThrPromet 499
Db      1324  GCTCCTCTC 1332

RESULT 8
US-09-013-118-2
; Sequence 2, Application US/09013118
; Patent No. 6503708
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: MICROTUBULE-ASSOCIATED PR
; TITLE OF INVENTION: OREIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013.118
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0464 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT02
; CLONE: 1312429
; US-09-013-118-2

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Pred. No.:	4.63e-11	Length:	2100
Score:	190.50	Matches:	91
Percent Similarity:	34.52%	Conservative:	55
Best Local Similarity:	21.51%	Mismatches:	138
Query Match:	7.22%	Indels:	139
DB:	4	Gaps:	17

US-09-315-355C-10 (1-501) x US-09-013-118-2 (1-2100)

QY	132	LeuYsAspThrGluGlnTyrGluArgGlu-----	-AspPheLeuIleYs-----	146
DB	319	CTTAAAGGCAAAATAGGTTCCACAAACATGTGAGTTGATTTCTTATTAAGGGCCAG		378
QY	147	-----ProSerAspAsnLeuIleValCysGlyArgAlaGluGlnAspGlnCys		162
DB	379	TTTCTGCGAATGCCCTTGACAAA-----	-CACATGAAATGGAGACGTC	423
QY	163	AsnLeuGlu-----	-ValHisValTyrAsnGlnGluAspSer	175
DB	424	TCATCAGAGAAAGTTGCGAAATAGTAATAGCTGGAGAGATATCTGCACCCCGACGACAG		483
QY	176	PheTyrValHisHisAspIleLeuLeuSerAlaTyrProLeuSerValGluTTPLeuAsn		195
DB	484	CAATGCATGTTCCATGATGACTGATGATTCATTAAAGGGCAGAGGAATG-----		537
QY	196	PheAspProSerProAspAspSerThnGlyAsnTyrIleAlaValGlyAsnMetThrPro		215
DB	538	-----	-ACTTGACTGATCTTATGATAG	561
QY	216	ValIleGluValTyrAspLeuAspIleValAspSerLeuGluProValPheThrLeuGly		235
DB	562	ACTTCTCGGATCTGCTCTTGAA-----		585
QY	236	SerIysLeuSerIysLysLysLysGlyLysLysSerSerAlaGluGlyHis		255
DB	586	-----	-GGAAGTCATTAATGACATTTGTGGACAT	615
QY	256	ThrAspAlaValIleuAspLeuSerTTPAsnLys-----	-LeuIleArgAsnValLeuAla	273
DB	616	ACGGATGTTGTAAGAGATGGCCGTGGTGAAGAAAGATAGTTTGCTCGCTTAATTTATG		675
QY	274	SerAlaSerAlaAspAsnThrValIleLeuTyrAspMetSerLeuGlyLysProAlaAla		293
DB	676	AGTGCCTTATGATCAGACTATTTCTCTTATGGAGCGAAT-----		717
QY	294	SerLeuAlaValHisThrAspLysValGlnThrIleu-----	-GlnPheHisProPhe	310
DB	718	-----	-GTAGAGAGAAACAAAGTGAAAGCCCTACACGTCTGTAGAGTCGTGGA	768
QY	311	GluAlaGlnThrIleu-----	-IleSerGlySerTyrAsp	321
DB	769	AGTGTAGATTCTATAGCTGTGATGCTCAGAACTAAATTTTGCAATGGCTCGTGGAT		828
QY	322	LysSerValAlaLeuTyrAspCysArgSerProAspGlnSerHisArgMetTyrArgPhe		341
DB	829	AAGATGCTAAAGATCTGGTCTACAGCTCCCTACAGATGAAGAAGTGAATG-----		879
QY	342	SerGlyGlnIleGluArgValThrTyrAsnHisAspSerProCysHisPheLeuAlaSer		361
DB	880	-----	-GAGGAGTCCACA-----	891
QY	362	ThrAspAspGlyPheValTyrAsnLeuAspAlaArgSerAspLys-----		376
DB	892	-----	-AATCGACCAAGAAAGAAACAGAAAGACAGAACACTTGGGA	930
QY	377	-----	-ProIlePheThrLeuAsnHisHisAsnAspGluIleSerGlyLeuAsp	392
DB	931	CTAACAGAGACTCCCATATGACCCCTCTCTGGCCACATGGAGGCGAGTTTCTCTCAGTTCTG		990
QY	393	LeuSerSerGlnIleTyrGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIle		412
DB	991	TGTCAGATGCTGAAGAAATCTGC-----	-AGTCATCTTGGGACCATACAAATTAGAGTG	1044


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217  eglValTrpAspLeuAspIleValAspSerLeuGluProValPheThrLeuGlySer 237
    : : : : :
1:050  AAAAGTTGG-----AGTACTGTAGT----- 1071
Oy 237  sLeuSerLysLysLysLysGlyLysLysSerSerSerAlaGluGlyIleThrAs 257
Db -----GGTTCACTTCTTCATCACTTCAAGGACATCTTC 1106
Oy 257  pAlaValLeuAspLeuSerTrpAsnLysLeuIleArgAsnValLeuAlaSerAla 277
Db 1107  CACTGTTCGATGCATGCGCT-----ATGGCTGGTTCCACTTGTCACTGCATCAG 1157
Oy 277  aAspAsnThrValIleLeuTrpAspMetSerLeuGlyLysProAlaIleSerLeuAla 297
Db 1158  AGATACCACTCTCTCGTATGGAGAGTGGATCCGAGCTCAGCTCGGACACTTATCATG 1217
Oy 297  IHisThrAspLysValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIle 317
Db 1218  CCATCATCAGCCGCTTCATGCGTTCAA-----TTCCGATGGAMACACTGTTGTTTC 1268
Oy 317  rGlySerTrpAspLysSerValAlaLeuThrAspCysArgSerProAspGluSerHis 337
Db 1269  GGGAGGATATGATTTTACCCTAAATTT----- 1298
Oy 337  gMetTrpArgPheSerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCys 357
Db 1297  -----TGGAAT----- 1302
Oy 357  sPheLeuAlaSerThrAspAspGlyPheValItyrAsnLeuAspAlaArgSerAspLys 377
Db 1303  -----GCTCATCTGGGAGATG 1319
Oy 377  oIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSerGln 397
Db 1320  TATCCGTACTCTGACCGGCTATAAATAAGATTTATTTCTCTTCTTTGAAAGCAG-- 1377
Oy 397  eLysGlyCysLeuValThrAlaSerAlaAspLysItyrValLysIleTrpAsp----- 414
Db 1378  CGATCGATCGTGTCTGTGGCTCTCGAGACACTTCATTTGCGGTGGATTTTACAG 1438
Oy 415  -----IleGluLysAspArgProSerLeuValHisSer 426
Db 1437  ACCGGAAGCCAGATGTGTGCTCTTTTGGACAGACACCTCATTTATATCCGGAT 1498
Oy 426  gAspMetLysMetGlyValLeuPheCysSerSerCysCysProAspLeuProPheIle 446
Db 1497  GCAATTCGAGGCAATATTTCTGTG-----TCATTCGATGCAGAT----- 1538
Oy 446  rAlaPheGlyGlnLysGluGlyLeuArgValTrpAspIleSerThrValSerSerVal 466
Db 1537  -----AGCGATGTAAAGTATGGATATTTCAGAGGAACTTGTGT 1577
Oy 466  lAsnGluAlaPheGlyArgGluArgLeu 476
Db 1578  ACACATGCTTCTGACATCGATCCGCTATC 1608

RESULT 11
US-09-356-952-12
; Sequence 12, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Boriack-Sjodin, Ann
; APPLICANT: Margalit, S. M.
; APPLICANT: Bor-Sogei, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: 600-1-228F
; CURRENT APPLICATION NUMBER: US/09/356, 952
; CURRENT FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 60/093, 631

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	EARLIER FILING DATE: 1998-07-21	
	NUMBER OF SEQ ID NOS: 14	
	SOFTWARE: PatentIn Ver. 2.0	
/	SEQ ID NO 12	
/	LENGTH: 43676	
/	TYPE: DNA	
-	ORGANISM: Saccharomyces cerevisiae	
US-09-356-952-12		
 Alignment Scores:		
Pred. No.:	1.12e-07	Length: 43676
Score:	179.00	Matches: 75
Percent Similarity:	40.54%	Conservative: 60
Best local Similarity:	22.52%	Mismatched: 129
Query Match:	6.78%	Indels: 69
DB:	3	Gaps: 14
 US-09-315-355C-10 (1-501) x US-09-356-952-12 (1-43676)		
Oy	167 HisValTyr AamGluGluAaspSerPheTyValHisHisAspIleLeuLeuSerAl	186
Db	16478 CAGGTCTACAGAGAAGAAATTGGTTCCITTAAGCGGCATTTATGCAGCTGTTACTGCT--	16535
Oy	186 aTyProLeuSerValGIUTrpleuasnPhE--AspProSerProaspSerpThxGl	205
Db	16536 -----CTTGtGTACACACGCCCTCGTTTCATGACAAGAGCCAGATTGAAGGCCA	16588
Oy	205 yaenTyrlleAlaValGlyAsnMetThrProValIleglValITrpaPleuAspIleVa	225
Db	16589 AAATTTATGTATCTTGTGCAGTGATGACAAAACCTGCACGATATGCTCAATAATGTTGA	16648
Oy	225 lApserLeuGIUProValPheThrLeuGlySerLySleuSerLySylValYblyBl	245
Db	16649 TGAAT-----TACTCATATAAACTCCAAGTCA	16675
Oy	245 sGIyLySerSerSerSerAlagIugLyHIsThrAspAlaValLeuAspLeuSerTrpas	265
Db	16676 TAACGACTCCGTTACTACAGAGAAGT-----	16703
Oy	265 nLySleuIleArg-----	269
Db	16704 ----TTGATTCGTACTTTGACCGGTGAATCTGCATTTCAAGGTATCGATTCCACAGAGA	16759
Oy	270 ----AsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuTrpaSerpMetSerIe	288
Db	16760 AAACTCCACGTTGCCACAGGTGGGCC----AAGATTCATCTTTGGACGTTAACG	16813
Oy	288 uGIyLyProAlaAlaSerLeuAlaValHisThrAspLySylValGlnThrLeuGlnPheH	308
Db	16814 ATTAGAACCCAGTTTCCGATCTATCATCGGGAGCACAGCAACATTACTAGTTTAAATTCAA	16873
Oy	308 sProphegluaIaGlnThrLeuIleSerGlySerTyraSpLySserValAlaLeuTyrs	328
Db	16874 TCMAATGAAGAACAGATATCTGGCCAGTACGTGATGATGAATTAATTCATTGTTCTTACGA	16933
Oy	328 pCySaYgSerProaspGlnSerHisArgMetTrpaGlyPheSerGlyGlnIleGIuArgYa	348
Db	16934 CTTAGAGAACCACTCCCCACAAAGAGATTGTTCAA--ACAAATGACGACGAATGCTAT	16990
Oy	348 lTrpTrpaAsnHisPheSerProcyHisIshPheLeuAlaSerTrpaAspGlyPheValTy	368
Db	16991 TTGCTGGAAATCCATGAGAGCCCTTCAACTTTGTACTGGCAATGAAGATCATACGCCCTTA	17052
Oy	368 rAmLeuAspAlaArgSerAspLySproIlePheThrLeuAsnAlaHisAsnAspGluIl	388
Db	17051 CTATATATGATATAGAGATTTATCAAGT-----TCATGATATGATTCAAAGATCAAGT	17104
Oy	388 eSerGly---LeuAspLeuSerSerGlnIleSylGlyCyS---LeuValIThrAlaSerAl	406
Db	17105 CACGCGAGTATAGATGTTGACTTTTCTCTCAACGCGGGATGAGATGTTCACGTTCGTGTA	17164
Oy	406 aaApLyTyTYValLyIleITrpAspIleLeuGlyAspArgProSerLeuValHisSerAr	426

Mon Feb 2 10:52:38 2004

us-09-315-355c-10.p2n.rn1

Page 11.

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Db      17165 CGATTAGAGTATCAGATATAT-----AAGACGAATCAGCAGATTGAG 17209
Qy      426 gaSPMeT-----lysMetGlyValIleuPheCyseSerCyScysProaSPLe 442
      17210 AGAATTATCATCATCAGAAAGAAATGACGATGTTTCCAGTTAAATATTCATGATTC 17269
Qy      442 uPProPheIleTyRAlaPheGlyGlyGlnLysGluGly-----LeuAr 456
      17270 TAAATATATTT-----ATCAGTGGATCTGATGATGAGGAAATGTTAGGCTATGAGAAAGTAA 17323
Qy      456 gValTTrpAspIleSerThrValIleSerSerValaAsnGlu 468
      17324 AGCTTGGAGAGGCTTAATGTCAAACTACTCTGTA 17360

RESULT 12
US-08-965-600-2
; Sequence 2, Application US/08965600
; Patent No. 6077688
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Puri
; TITLE OF INVENTION: NEW TRANSDUCIN BETA-1 SUBUNIT
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,600
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0416 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1221 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 194046
; US-08-965-600-2

Alignment Scores:
Pred. No.: 4.2e-10 Length: 1221
Score: 178.50 Matches: 77
Percent Similarity: 41.43% Conservative: 56
Best Local Similarity: 23.99% Mismatches: 125
Query Match: 6.75% Indels: 63
DB: 3 Gaps: 15

US-09-315-355C-10 (1-501) x US-08-965-600-2 (1-1221)

Qy      168 ValTyRAsnGlnGluIleuAspSerPheTyRValHisHisAspIleLeuLeuSerAlaTyR 187
      101 CTCTTAAACCAAGAGCA-----GCCCATGATGATGCCAT 136
Qy      188 ProLeuSerValGluIleuAsnPheAspProSerProAspAspSerThrGlyAsnTyR 207
      137 ---TGTCAGTTCCTTGG-----GGACAAACAAGAGAAACTGTGAGACA 181
Qy      208 IleAlaValGlyAsnMetThrProValIleGluValTyRAspLeuAspIleValaSPser 227
      182 GTGTGACAGAGCTCCCTAGATGACCTGTGAGAGCTGTGG----- 220
Qy      228 LeuGluProValPheThrLeuGlySerLysLeuSerLysLysLysLysGlyLys 247
      221 -----AAATGGCGTGTGAGAGCTGTGAC 244
Qy      248 LysSerSerSerAlaGlnGlyHisThrAspAlaValIleuAspLeuSerTrpAsnLysLeu 267
      245 CTACAGTGGAGTGTGAGGAGCAATCAGCTGGAGAGTGTGTGTGACATCGCACACACC 304
Qy      268 IleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuTyRAspMetSer 287
      305 CTG---CCCATTCCTGATCCAGCTCTTGTATGCTCATATTCCTTTGGAGCTTGAA 361
Qy      288 LeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeuGlnPhe 307
      362 AATGGCAACAGATAAATGTCATGATGACGAGCTGTGATGCTGTGACTTGGCTTT 421
Qy      308 HisProPheGluAlaGlnThrLeuIleSerGlySerTyRAspLysSerValAlaLeuTyR 327
      422 TCTCTCT---GATTCACAGATCTGGCCACAGAACTCATGTGCGGAAGTGAACATTTT 478
Qy      328 AspCysArgSerProAspGluSerHisArgMetTrpArgPheSerGlyGlnIleGluArg 347
      479 GGTGTGAAGAGTGGAAAAAGAAATATCTTTGGACACAGAGAAATTCATTCTTAGT 538
Qy      348 ValThrTrpAsnHisPheSerPro---CysHisPheLeuAlaSer---ThrAspArgIly 365
      539 ATTGCA-----TATAGTCTGTGATGGGAATTAACCTAGCCAGTGGAGCCATATGGA 589
Qy      366 PheValTyRAsnLeuAspAlaArgSerAspLysProIlePheThrLeuAsnAlaHisAsn 385
      590 ATCATCAATATTTTATATATTCGAACTGGAAACTTCTGATACCTCTGGAAGCCATGCC 649
Qy      386 AspGluIleSerGlyLeuAspLeuSer-----SerGlnIleLysGlyCysLeuValThr 403
      650 ATGCCCATTCGCTCTTGACCTTTTCCCGGACTCCAGCTC-----CTTGTCACT 700
Qy      404 AlaSerAlaAspLysTyRValIlyValIleTyRAspIle----- 415
      701 GCTTCAGATGATGGCTACATCAAGATCTATGATGATCAACATGCCAATTTGGCTGGCAGC 760
Qy      416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValIleuPheCys 435
      761 CTGAGCGGCGCATCCCTCTGGGTG-----CTGAACGTTGATTCCTGT 802
Qy      436 SerSerCysCysProAspLeuProPheIleTyRAlaPheGlyGlyGlnLysGluGlyLeu 455
      803 CTTGAT-----GACACTCACTTGTGTTCCAGT-----TCGTCTGACAAAGTGA 847
Qy      456 ArgValTyRAspIleSerThrValSerSerValaAsnGluAlaPheGlyArgArgGluArg 475
      848 AAAGTTGGGATGTGGAACGAGAGACTGTGTTTCAACACTTCTTTATATCCAGGATCAG 907
DB: 476 Leu 476
DB: 908 GTC 910

RESULT 13
US-09-489-506-2
; Sequence 2, Application US/09489506
; Patent No. 6465619
; GENERAL INFORMATION:

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; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620.312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 411
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)..(1455)
US-09-620-312D-411

Alignment Scores:
Pred. No.: 1,19e-09 Length: 2338
Score: 178.50 Matches: 105
Percent Similarity: 32.23% Conservative: 61
Best Local Similarity: 20.39% Mismatches: 207
Query Match: 6.76% Indels: 143
DB: Gaps: 19

US-09-315-355c-10 (1-501) x US-09-620-312D-411 (1-2338)

QY 19 LysGluThrProAspLysValGluLeu-----SerLysGluGluValLysArgLeu 35
DB 59 AAGGAAACCCGGAAGTACGCTTACCGGCTGTCAAGCAGAGAGGTTGGAAGTGC- 117
QY 36 IleAlaGluAlaLysGluLysLeuGluGluGluGluGluGluGluGluGluGluThr 55
DB 118 GCGGCGCGCAAGGTCGCGCTGCACTGTGAACCGGGAACCCATGGAAGCCGAGTCC 177
QY 56 GlySerProSerGluAspGlyMetGlnSerAlaArgThrGlnAlaArgProArgGluPro 75
DB 178 GGGGACACAGTTCGAGAGGCGCGCCGACAGTCACTGCGCGCGCGG---GGGCGCGG 234
QY 76 LeuGluAspGluAspProGluAspAspArgThrLeuAspAspGluLeuAlaGluTyr 95
DB 235 CTACGCGAAGGG-----GAGGAGCTGTGATGACGAGGAGGCGCTATGCTCTAC 285
QY 96 -----AspLeuAspLysTyrAspGluGlu 103
DB 286 CACGAGCGAGACTGCGCCCTGTCTCAGCTTTCATATGATGCCG---GATCAGCTG 342
QY 104 GlyAspProAspAlaGlu-----ThrLeuGlyGlu 113
DB 343 GGAAGACACCGGACAGAGCTTCCCTTACACTTTCCTGTCTGGAGCCGAGCTGAG 402
QY 114 Ser-----LeuLeuGlyLeuThrValTyrGlySerAsnAspGlnAspPro 128
DB 403 AGCCCCAGAGCAACAGACTGATGCTTCGATGCAATCGCATGGGACAAAGCCC 462
QY 129 TyrValThrLeuLysAspThrGluGlnTyrGluArgLysAspPheLeuLysProSer 148
DB 463 CCACCCCTCAGAGGCGAGTGTGAAGAAAGAGAGAGAGAT----- 504
QY 149 AspAsnLeuLeuValCysGlyArgAlaGluGlnAspGlnCysAsnLeuGluValIleVal 168
DB 504 ----- 504
QY 169 TyrAsnGlnGluAspSerPheTyrValHisAspIleLeuLeuSerAlaTyrPro 188
DB 505 -----GAAAGAGATGAAGAGAGGAAACCTCAGCTGGAGCTGGCCATGTCGCC 555
QY 189 -----LeuSerValGluTyrLeuAsnPheAspProSerProAsp 201
DB 556 CACTATGCTGCATCAACCGAGTTCGGGTTCATGTCAGCTGGGTGAAGG----- 603
QY 202 AspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGluValTyrAsp 221

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DB 604 -----CTGTGCTGCGGGGTGTCTA 624
QY 222 -----LeuAspIleValAspSerLeu 228
DB 625 GAAAGAGCCAGGTGAGAGTGTTCGCGCGGCTTCTGACAGTGTGAGAGAGCCC 664
QY 229 GluProValPheThrLeuGlySerLysLeuSerLysLysLysLysLysLysLys 248
DB 685 CAGGCCCTG-----GCAGCTTCCTCCGGAGATGAGCAGGCCCAATGAAAGCCC 732
QY 249 SerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTrpAsnLysLeuIle 268
DB 733 ATCTTCTCTTCCTGCTGACACATGAGCGAGGCTTTCCTTCATGCTGCTCCCGCGGTG 792
QY 269 ArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuThrPaspMetSerLeu 288
DB 793 ACCGTCGCTGCTGACCGGTGACTCTCAAAAGACATCCACTGAGACCTTACGAG 852
QY 289 Gly-----LysProAlaAlaSerLeuAlaValHisThrAspLys 301
DB 853 GGGGCTCTGCGACGTGAGCAGCGGCCATTCGTGGG-----CACACACGCTCT 903
QY 302 ValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuLysSerGlySerTyrAsp 321
DB 904 GTGAGAGACCTGACGTGATCAGCAGCTGACCAACACCGGTGTTTCTCTGCTGAGTGC 963
QY 322 LysSerValAlaLeuTyrAspCysArgSerProAspGluSerHisArgMet----- 338
DB 964 GCCTTCATCCGATCTGGGACATCCGAGCAGCCGCCCAAGAGGCTGCATGCTCACCA 1023
QY 339 ---TrpArgPheSerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHis 357
DB 1024 GCGACGCGCCATATGGGAGCGTCATGTCATGATGAGCGCGCGGAGGCC---TTC 1080
QY 358 PheLeuAlaSerThrAspAspGlyPheValTyrAsnLeuAspAlaArg-----Ser 374
DB 1081 CTGCTCAGTGGCGGAGTATGATGAGGCGCTTCATGATCTGGGACCTTGGCAGTTC 1140
QY 375 AspLysProIlePheThrLeuAsnAlaHisAsnAspGluLysSerGlyLeuAspLeuSer 394
DB 1141 GGTTCCTCCAGTGGCCACCTTCAAGCAGCAGTGGCCCGCTGCTCCGAGTGGCAC 1200
QY 395 SerGlnIleLysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleTyrAsp 414
DB 1201 CCCAGAGACGCGGGGTCTTGCAGCCTCGGGTGCAGACCAACATCAACAGCTGGAC 1260
QY 415 Ile-----LeuGlyAsp 418
DB 1261 CTGGCAGTGGAGCGGAGCCCTGAGCGGGCGACGTGAGAGCGACCCCGGACTGGCGAC 1320
QY 419 ArgProSer-----LeuValHisSerArgAspMetLysMetGlyValLeuPheCys 435
DB 1321 CTCCTCCGAGCAGCTGTCTGTCGACACAGGCGAAGCCAGAGCTGAAGAGCTGCG 1380
QY 436 SerSerCysCysProAspLeuProPheIleTyrAlaPheGlyGly 450
DB 1381 CACCCGAGTGCACAGGCTCTCTGTCAGCAGCGCGCTGTCAAGGC 1425

RESULT 15
US-09-108-857-1
; Sequence 1, Application US/09108857A
; Patent No. 6433137
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Alexander D.
; APPLICANT: BRAUN, Burkhard
; TITLE OF INVENTION: TUP1 SEQUENCES FROM CANDIDA ALBICANS AND METHODS FOR
; TITLE OF INVENTION: SCREENING AGENTS FOR INHIBITING VIRULENCE IN CANDIDA
; TITLE OF INVENTION: ALBICANS USING TUP1
; FILE REFERENCE: 22002-20006.00
; CURRENT APPLICATION NUMBER: US/09/108.857A
; CURRENT FILING DATE: 1998-07-01
; EARLIER APPLICATION NUMBER: 60/051,552

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EARLIER FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 2272
 TYPE: DNA
 ORGANISM: Candida albicans
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (337)..(1878)
 US-09-108-857-1

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	4.07e-09	2272	115	73	181	165
Percent Similarity:	173.50					
Best Local Similarity:	35.21%					
Query Match:	21.54%					
	6.57%					

US-09-315-355c-10 (1-501) x US-09-108-857-1 (1-2272)

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QY 26 GluLeuSerLysGluValLysArgLeuIleAlaGluAlaLysGluLysLeuGlnGlu 45
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Db 550 GAGGCATACGAGAGATATTGAGGTTAAAGACGAGTTGACACTAGACAGACGAA 609
QY 46 GluLysGlySerAspGluGluThrGlySerProSerGluAspGlyMetGlnSer 65
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Db 610 ATGAAGATGGCTTCCAAACAACAACGACACGACAAACGACAAACGACGAG 669
QY 66 AlaArgThrGln-----AlaArgProArgGluProLeuGluAspGlyAspProGlu 82
   |||
   |||
   |||
Db 670 CAGCAACAACAAGATTGTGGACCAACCTCGCCGACCTGCTCCACCAACCCG--- 726
QY 83 AspAspArgThrLeuAspAspAspGluLeuAlaGluTyrAspLeuAspLysTyrAspGlu 102
   |||
   |||
   |||
Db 726 ----- 726
QY 103 GluLysAspProAspAlaGluThrLeuGlyLeuSerLeuGlyLeuThrValTyrGly 122
   |||
   |||
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Db 727 -----GTCACATCTATTTCG 741
QY 123 SerAsnAspGlnAspProTyrVal-----ThrLeuLysAspThrGluGlnTyrGlu 139
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   |||
   |||
Db 742 GTATTCGACAGTACATACATATGTCACACCCCAAGAGGTAACGACGACGAA 801
QY 140 ArgGluAspPheLeuIleLysProSerAspAsnLeuIleValCysGlyArgAlaGluGln 159
   |||
   |||
   |||
Db 802 ATCCCAACCATCTTG-----CAAGATTAGACATTGCCAAAGCCCAACCCGAGTTC 852
QY 160 AspGlnCysAsnLeuGluValHisVal-----TyrAsnGlnGluGluAsp 174
   |||
   |||
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Db 853 AAGAAACAGCACCTCGAATACTATGTGTGTACAAACCCAGCGTCTCCAAAGACTTGAT 912
QY 175 SerPheTyrValHis-----HisAspIleLeuSerAlaTyrProLeuSerVal 191
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Db 913 ATTGACATGCTCCACTCTTAGACCACTGTCAGTGTTCCTGCTGAGATTTCCAGA 972
QY 192 GluTyrLeuAsnPheAspProSerProAspAspSerThrGlyAsnTyrIleAlaValGly 211
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Db 973 GAC-----GGCAAGTTTCATCGCCACCGGT 996
QY 212 -----AsnMetThrProValIleGluValTyrAspLeuAspIleValAspSerLeuGlu 229
   |||
   |||
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Db 997 TGCACAAACACCCCAAGTTCATGTCACACCGGAGAGTGTGTC----- 1044
QY 230 ProValPheThrLeuGlySerLysLeuSerLysLysLysLysLysLysSer 249
   |||
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Db 1045 -----GCCAATTTGATTGACGAGTCTCCCAACGAAACAA----- 1080
QY 250 SerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTyrAsnLysLeuIleArg 269
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Db 1081 -----GACGACAAACACCCGCTCAGGCGACTTG-----TACATCGA 1119
  
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QY 270 AsnVal-----LeuAlaSerAlaSerAlaAspAsnThrVal 281
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Db 1120 TCTGTGTGTTTCCCTGACGGAACCTTGGCCAGAGTCACAGACGAGTGTGAT 1179
QY 282 IleLeuTyrAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLys 301
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   |||
Db 1180 AGAATCTGGGATTGAGCACAAAGAGAAATTAATCTTGGGGGCGGACGAAACAGAC 1239
QY 302 ValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerTyrAsp 321
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   |||
Db 1240 ATTTACTGTTAACTTTTCCCT---GATGGGATAGTGTGTTCCAGCTCCGGCGAT 1296
QY 322 LysSerValAlaLeuTyrAspCysArg----- 330
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Db 1297 AGGTCAAGTCAAGATCTGGGACTTGAAGACCTCCAGGTCTCTTGACTTGTGATCGAA 1356
QY 331 -----SerProAspGluSerHisArgMetTyrAspPheSer 342
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   |||
   |||
Db 1357 GACGGCGTCAACCAACCGGCGCTCTCCCGGACGGA-----CTCATGTCTGCC 1407
QY 343 GlyGlnIleGluArgVal-----ThrTyrAsnHisPheSerProCysHisPheLeuAla 360
   |||
   |||
   |||
Db 1408 GGCTCATTTAGATGAACCGTTAGAGTGTGGAC----- 1440
QY 361 SerThrAspAspGlyPheValTyrAsnLeuAspAlaArgSerAspLysProIlePheThr 380
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Db 1441 TCACACTACGGGTTCTTGGTTCGACACGCTTAGATCCGGGCAACGAAACGCGC----- 1491
QY 381 LeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerGlnIleLysGlyCys 400
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Db 1492 ---AATGGCCACAAAGATCTAGCTCTGCTCTCTCCAAACAACGCGCAACA--- 1545
QY 401 LeuValThrAlaSerAlaAspLysTyrValLysIleTyrAspIleLeuGly-----Asp 418
   |||
   |||
   |||
Db 1546 ATGCTTCCGGGCTCTTAGACAGAACCGTCAAGTGTGGACCTTGGCAAGCAAGTCCGAC 1605
QY 419 ArgProSer-----LeuValHisSerArgAspMetLysMetGlyValLeu 433
   |||
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Db 1606 AAAAAGTCGACCTCGGAGTACCTTACCTTGGCCACAGACCTTGTGTGCGGTC--- 1662
QY 434 PheCysSerSerCysCysProAspLeuProPheIleTyrAlaPheGlyGlnLysGlu 453
   |||
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   |||
Db 1663 -----TGCTGTACCCCGGACAAAGATCATTTTGTGCG---GGCTCAAGGACCGT 1710
QY 454 GlyLeuArgValTyrAspIleSerThrValSerSerValAsnGluAlaPheGlyArgArg 473
   |||
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Db 1711 GGTCATTTTCTGGGAC-----CAAGCTTCAAGT---AAC 1743
QY 474 GluArgLeuValLeuGlySerAlaArgAsnSerSerIleSer----- 487
   |||
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   |||
Db 1744 CCAATTGTGATTGTCAGGGGCAACCGCACTCGTATCTCACTCGCTGATCCCTTAAC 1803
QY 488 -----GlyProPheGlySerArgSerSerAsp 496
   |||
   |||
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Db 1804 TCAAGGGAACGAAAGTATCTTCGCTACAGTAGTGGCGAT 1845
  
```

Search completed: January 31, 2004, 04:27:38
 Job time : 142 secs

From: Chan, Christina
Sent: Thursday, January 29, 2004 11:25 AM
To: Holleran, Anne; STIC-Biotech/ChemLib
Subject: RE: RUSH search for 09/315,355

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Holleran, Anne
Sent: Thursday, January 29, 2004 10:36 AM
To: Chan, Christina
Subject: RUSH search for 09/315,355

Please approve and forward to STIC the following RUSH sequence search. This is for an amendment due this biweek. Thanks.

Please search the following in the interference search databases:

1. polynucleotides that encode SEQ ID NO: 10
2. oligomer search of polynucleotides that encode SEQ ID NO: 10

Anne Holleran
AU: 1642
Tel: 308-8892
RM: 8e03

mailbox: 8e12

After Jan. 30:

Tel: 571 272-0833
RM: Remsen, 3A14

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 2/2
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

